

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Goodman, Corey S.
Kidd, Thomas
Mitchell, Kevin
Tear, Guy

(ii) TITLE OF INVENTION: Robo: A Novel Family of Polypeptide and
Nucleic Acids

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
(B) STREET: 75 DENISE DRIVE
(C) CITY: HILLSBOROUGH
(D) STATE: CALIFORNIA
(E) COUNTRY: USA
(F) ZIP: 94010

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: OSMAN, RICHARD A
(B) REGISTRATION NUMBER: 36,627
(C) REFERENCE/DOCKET NUMBER: B98-006

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (650) 343-4341
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4188 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| ATGCATCCCA | TGCATCCCGA | AAACCACGCC | ATCGCCCGGA | GCACGAGCAC | CACTAATAAC | 60 |
| CCATCTCGCA | GTCGGAGCAG | CAGGATGTGG | CTCCTGCCCC | CCTGGCTGCT | CCTCGTCCTG | 120 |
| GTGGCCAGCA | ATGGCCTGCC | AGCAGTCAGA | GGCCAGTACC | AATCGCCACG | TATCATCGAG | 180 |
| CATCCCACGG | ATCTGGTCTG | TAAGAAGAAT | GAACCCGCCA | CGCTCAACTG | CAAAGTGGAG | 240 |
| GGCAAGCCGG | AACCCACCAT | TGAGTGGTTT | AAGGATGGCG | AACCCGTCAG | CACCAACGAA | 300 |
| AAGAAATCGC | ACCGCGTCCA | GTTCAAGGAC | GGCGCCCTCT | TCTTTTACAG | GACAATGCAA | 360 |
| GGCAAGAAGG | AGCAGGACGG | CGGAGAGTAC | TGGTGCCTGG | CCAAGAACCG | AGTGGGCCAG | 420 |
| GCCGTTAGTC | GCCATGCCTC | CCTCCAGATA | GCTGTTTTGC | GCGACGATTT | TCGCGTGGAG | 480 |
| CCCAAAGACA | CGCGAGTGGC | CAAAGGCGAG | ACGGCTCTGC | TGGAGTGTGG | GCCGCCCAAA | 540 |
| GGCATTCCAG | AGCCAACGCT | GATTTGGATA | AAGGACGGCG | TTCCCTTGGA | CGACCTGAAA | 600 |
| GCCATGTCTG | TTGGCGCCAG | CTCCCGCGTT | CGAATTGTGG | ACGGTGGCAA | CCTGCTGATC | 660 |
| AGCAATGTGG | AGCCCATTTG | TGAGGGCAAC | TACAAGTGCA | TTGCCCAGAA | TCTGGTAGGC | 720 |
| ACCCGCGAGA | GCAGCTATGC | CAAGCTGATT | GTCCAGGTCA | AACCATACTT | TATGAAGGAG | 780 |
| CCCAAGGATC | AGGTGATGCT | CTACGGCCAG | ACAGCCACTT | TCCACTGCTC | AGTGGGCGGT | 840 |
| GATCCGCCGC | CGAAAGTGTT | GTGGAAAAAG | GAGGAGGGCA | ATATTCCGGT | GTCCAGAGCG | 900 |
| CGAATCCTTC | ACGACGAGAA | AAGTTTAGAG | ATATCCAACA | TAACGCCCAC | CGATGAGGGC | 960 |
| ACCTATGTCT | GCGAGGCACA | CAACAATGTC | GGTCAGATCA | GCGCTAGGGC | TTCTCTTATA | 1020 |
| GTCCACGCTC | CGCCGAACCT | TACGAAAAGA | CCCAGTAACA | AGAAAGTGGG | ACTAAATGGG | 1080 |
| GTTGTCCAAC | TACCTTGCAT | GGCCTCCGGA | AACCCTCCGC | CGTCTGTATT | CTGGACCAAG | 1140 |
| GAAGGAGTAT | CCACTCTTAT | GTTCCCAAAT | AGTTCGCACG | GAAGGCAGTA | TGTGGCTGCC | 1200 |
| GATGGAACCT | TGCAGATTAC | GGATGTGCGG | CAGGAAGACG | AAGGCTACTA | TGTGTGTTCC | 1260 |
| GCTTTCAGTG | TAGTCGATTC | CTCTACAGTA | CGGGTTTTTC | TGCAAGTCAG | CTCGGTAGAC | 1320 |
| GAGCGTCCAC | CTCCGATTAT | TCAAATCGGA | CCTGCCAATC | AAACACTGCC | CAAGGGATCA | 1380 |
| GTTGCTACTT | TACCCTGTCT | GGCCACTGGA | AATCCCAGTC | CCCGTATCAA | GTGGTTCCAC | 1440 |
| GATGGACATG | CCGTACAAGC | GGGCAATCGA | TACAGCATCA | TCCAAGGAAG | CTCACTGAGA | 1500 |
| GTCGATGACC | TTCAACTAAG | TGACTCTGGT | ACCTACACCT | GCACTGCATC | TGGCGAACGA | 1560 |
| GGAGAAACTT | CCTGGGCTGC | CACACTAACG | GTGGAAAAAC | CCGGTTCTAC | ATCTCTTCAC | 1620 |
| CGGGCAGCTG | ATCCTAGCAC | TTATCCTGCT | CCTCCAGGAA | CACCTAAAGT | CCTGAATGTC | 1680 |
| AGTCGCACCA | GCATTAGTCT | TEGTTGGGCT | AAAAGCCAAG | AGAAACCCGG | AGCTGTGGGC | 1740 |
| CCAATCATTG | GATACACTGT | AGAGTACTTC | AGTCCGGATC | TGCAAACTGG | TTGGATTGTG | 1800 |
| GCTGCCCATC | GAGTCGGCGA | CACTCAAAGT | ACTATCTCGG | GTCTCACTCC | TGGCACTTCG | 1860 |
| TATGTGTTCC | TAGTTAGAGC | TGAGAATACT | CAGGGTATTT | CTGTGCCTTC | CGGCTTATCA | 1920 |
| AATGTTATTA | AAACCATTGA | GGCAGATTTC | GATGCAGCTT | CTGCCAATGA | TTTGTGAGCA | 1980 |
| GCTCGAACTT | TGCTGACAGG | AAAGTCGGTG | GAGCTAATAG | ATGCCTCGGC | TATCAATGCT | 2040 |
| AGTGCCGTTA | GACTTGAGTG | GATGCTCCAC | GTGAGCGCTG | ATGAGAAATA | CGTAGAGGGC | 2100 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| CTGCGCATAC | ACTATAAGGA | TGCCAGTGTA | CCATCCGCAC | AGTATCACTC | GATCACTGTT | 2160 |
| ATGGATGCCT | CTGCAGAATC | GTTTGTGGTG | GGAAACCTTA | AGAAGTACAC | CAAGTATGAG | 2220 |
| TTCTTCCTAA | CACCCTTTTT | TGAGACAATT | GAAGGACAGC | CCAGTAACTC | CAAGACAGCC | 2280 |
| CTCACCTATG | AAGATGTTCC | CTCCGCACCA | CCGGATAACA | TTCAGATTGG | CATGTACAAC | 2340 |
| CAAACAGCCG | GTTGGGTGCG | TTGGACTCCG | CCACCCTCCC | AGCACCACAA | TGGCAATTTG | 2400 |
| TATGGCTACA | AGATTGAGGT | CAGCGCCGGT | AACACCATGA | AGGTGCTGGC | CAATATGACT | 2460 |
| CTTAATGCTA | CCACCACATC | TGTGCTCCTA | AATAACCTAA | CCACCGGAGC | TGTGTACAGC | 2520 |
| GTGAGGTTGA | ACTCCTTTAC | CAAGGCAGGA | GATGGACCTT | ACTCCAAACC | GATATCACTA | 2580 |
| TTCATGGACC | CCACCCATCA | TGTGCATCCG | CCACGGGCAC | ATCCAAGCGG | CACCCATGAT | 2640 |
| GGGCGACATG | AGGGACAGGA | TCTCACGTAT | CATAACAATG | GCAACATACC | ACCTGGCGAC | 2700 |
| ATTAATCCCA | CCACTCATAA | AAAGACCACT | GACTACCTAT | CTGGACCGTG | GCTAATGGTG | 2760 |
| CTGGTCTGCA | TCGTTCTTCT | AGTCCTGGTT | ATTTCGGCGG | CTATTTCGAT | GGTCTACTTC | 2820 |
| AAGCGCAAGC | ATCAAATGAC | CAAGGAATTG | GGTCACTTAA | GTGTGGTCAG | TGACAACGAA | 2880 |
| ATAACCGCAT | TAAATATCAA | TAGCAAAGAG | AGCCTTTGGA | TAGACCATCA | TCGTGGATGG | 2940 |
| CGAACTGCCG | ATACTGACAA | AGACTCAGGA | TTAAGCGAAT | CGAAGCTACT | ATCCCACGTT | 3000 |
| AACAGCAGTC | AATCCAATA | CAATAACTCC | GATGGAGGAA | CCGATTATGC | AGAAGTTGAC | 3060 |
| ACCCGTAACC | TTACCACCTT | CTACAATTGT | CGCAAGAGCC | CCGATAATCC | CACGCCGTAC | 3120 |
| GCCACCACTA | TGATCATTGG | TACCTCTTCC | AGTGAGACCT | GCACCAAGAC | AACATCTATA | 3180 |
| AGTGCCGATA | AGGACTCGGG | AACTCATTCG | CCCTATTCTG | ACGCATTTGC | CGGTCAGGTG | 3240 |
| CCAGCGGTTT | CTGTTGTCAA | ATCCAACAT | CTTCAGTATC | CGGTTGAACC | GATCAACTGG | 3300 |
| TCAGAGTTTC | TACCCCCGCC | GCCAGAACAC | CCACCTCCGT | CTTCTACCTA | TGGATACGCA | 3360 |
| CAAGGATCTC | CTGAATCTTC | GCGGAAGAGC | TCCAAAAGCG | CAGGTTCCGG | CATTTCTACA | 3420 |
| AATCAAAGCA | TTCTGAACGC | ATCCATACAC | AGCAGCTCCT | CGGGCGGCTT | TTCAGCTTGG | 3480 |
| GGAGTATCGC | CCCAATATGC | TGTCGCCTGT | CCACCGGAAA | ACGTTTATAG | CAATCCGCTG | 3540 |
| TCGGCAGTGG | CTGGCGGCAC | CCAGAACCGC | TATCAGATAA | CGCCACAAA | CCAACATCCG | 3600 |
| CCACAGTTAC | CGGCCTACTT | TGCCACCACG | GGTCCAGGAG | GAGCTGTACC | ACCCAACCAC | 3660 |
| CTGCCATTTG | CCACACAGCG | TCATGCAGCC | AGCGAGTACC | AGGCTGGACT | GAATGCAGCG | 3720 |
| CGATGTGCC | AAAGCCGCGC | CTGCAACAGC | TGCGATGCCT | TGGCCACACC | CTCGCCCATG | 3780 |
| CAACCCCCAC | CGCCAGTTCC | CGTACCCGAG | GGCTGGTACC | AACCGGTGCA | TCCCAATAGC | 3840 |
| CACCCGATGC | ACCCGACCTC | CTCCAACCAC | CAGATCTACC | AGTGCTCCTC | CGAGTGCTCG | 3900 |
| GATCACTCGA | GGAGCTCGCA | GAGTCACAAG | CGGCAGCTGC | AGCTCGAGGA | GCACGGCAGC | 3960 |
| AGTGCCAAAC | AACGCGGAGG | ACACCAGCGT | CGACGAGCCC | CGGTGGTGCA | GCCGTGCATG | 4020 |
| GAGAGCGAGA | ACGAGAACAT | GCTGGCGGAG | TACGAGCAGC | GCCAGTACAC | CAGCGATTGC | 4080 |
| TGCAATAGCT | CCCGCGAGGG | CGACACCTGC | TCCTGCAGCG | AGGGATCCTG | TCTTTACGCC | 4140 |
| GAGGCGGGCG | AGCCGGCGCC | TCGTCAAATG | ACTGCTAAGA | ACACCTAA | | 4188 |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1395 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | His | Pro | Met | His | Pro | Glu | Asn | His | Ala | Ile | Ala | Arg | Ser | Thr | Ser | | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | | |
| Thr | Thr | Asn | Asn | Pro | Ser | Arg | Ser | Arg | Ser | Ser | Arg | Met | Trp | Leu | Leu | | |
| | | | | 20 | | | | 25 | | | | | 30 | | | | |
| Pro | Ala | Trp | Leu | Leu | Leu | Val | Leu | Val | Ala | Ser | Asn | Gly | Leu | Pro | Ala | | |
| | | | | 35 | | | | 40 | | | | 45 | | | | | |
| Val | Arg | Gly | Gln | Tyr | Gln | Ser | Pro | Arg | Ile | Ile | Glu | His | Pro | Thr | Asp | | |
| | | | | 50 | | | | 55 | | | | 60 | | | | | |
| Leu | Val | Val | Lys | Lys | Asn | Glu | Pro | Ala | Thr | Leu | Asn | Cys | Lys | Val | Glu | | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | | |
| Gly | Lys | Pro | Glu | Pro | Thr | Ile | Glu | Trp | Phe | Lys | Asp | Gly | Glu | Pro | Val | | |
| | | | | | 85 | | | | 90 | | | | 95 | | | | |
| Ser | Thr | Asn | Glu | Lys | Lys | Ser | His | Arg | Val | Gln | Phe | Lys | Asp | Gly | Ala | | |
| | | | | 100 | | | | 105 | | | | | 110 | | | | |
| Leu | Phe | Phe | Tyr | Arg | Thr | Met | Gln | Gly | Lys | Lys | Glu | Gln | Asp | Gly | Gly | | |
| | | | | 115 | | | | 120 | | | | 125 | | | | | |
| Glu | Tyr | Trp | Cys | Val | Ala | Lys | Asn | Arg | Val | Gly | Gln | Ala | Val | Ser | Arg | | |
| | | | | 130 | | | | 135 | | | | 140 | | | | | |
| His | Ala | Ser | Leu | Gln | Ile | Ala | Val | Leu | Arg | Asp | Asp | Phe | Arg | Val | Glu | | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | | |
| Pro | Lys | Asp | Thr | Arg | Val | Ala | Lys | Gly | Glu | Thr | Ala | Leu | Leu | Glu | Cys | | |
| | | | | | 165 | | | | 170 | | | | 175 | | | | |
| Gly | Pro | Pro | Lys | Gly | Ile | Pro | Glu | Pro | Thr | Leu | Ile | Trp | Ile | Lys | Asp | | |
| | | | | 180 | | | | | 185 | | | | 190 | | | | |
| Gly | Val | Pro | Leu | Asp | Asp | Leu | Lys | Ala | Met | Ser | Phe | Gly | Ala | Ser | Ser | | |
| | | | | 195 | | | | 200 | | | | | 205 | | | | |
| Arg | Val | Arg | Ile | Val | Asp | Gly | Gly | Asn | Leu | Leu | Ile | Ser | Asn | Val | Glu | | |
| | | | | 210 | | | | 215 | | | | 220 | | | | | |
| Pro | Ile | Asp | Glu | Gly | Asn | Tyr | Lys | Cys | Ile | Ala | Gln | Asn | Leu | Val | Gly | | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | | |
| Thr | Arg | Glu | Ser | Ser | Tyr | Ala | Lys | Leu | Ile | Val | Gln | Val | Lys | Pro | Tyr | | |
| | | | | | 245 | | | | | 250 | | | | | 255 | | |

| | | | |
|---|-----|-----|-----|
| Phe Met Lys Glu Pro Lys Asp Gln Val Met Leu Tyr Gly Gln Thr Ala | | | |
| 260 | 265 | 270 | |
| Thr Phe His Cys Ser Val Gly Gly Asp Pro Pro Pro Lys Val Leu Trp | | | |
| 275 | 280 | 285 | |
| Lys Lys Glu Glu Gly Asn Ile Pro Val Ser Arg Ala Arg Ile Leu His | | | |
| 290 | 295 | 300 | |
| Asp Glu Lys Ser Leu Glu Ile Ser Asn Ile Thr Pro Thr Asp Glu Gly | | | |
| 305 | 310 | 315 | 320 |
| Thr Tyr Val Cys Glu Ala His Asn Asn Val Gly Gln Ile Ser Ala Arg | | | |
| 325 | 330 | 335 | |
| Ala Ser Leu Ile Val His Ala Pro Pro Asn Phe Thr Lys Arg Pro Ser | | | |
| 340 | 345 | 350 | |
| Asn Lys Lys Val Gly Leu Asn Gly Val Val Gln Leu Pro Cys Met Ala | | | |
| 355 | 360 | 365 | |
| Ser Gly Asn Pro Pro Pro Ser Val Phe Trp Thr Lys Glu Gly Val Ser | | | |
| 370 | 375 | 380 | |
| Thr Leu Met Phe Pro Asn Ser Ser His Gly Arg Gln Tyr Val Ala Ala | | | |
| 385 | 390 | 395 | 400 |
| Asp Gly Thr Leu Gln Ile Thr Asp Val Arg Gln Glu Asp Glu Gly Tyr | | | |
| 405 | 410 | 415 | |
| Tyr Val Cys Ser Ala Phe Ser Val Val Asp Ser Ser Thr Val Arg Val | | | |
| 420 | 425 | 430 | |
| Phe Leu Gln Val Ser Ser Val Asp Glu Arg Pro Pro Pro Ile Ile Gln | | | |
| 435 | 440 | 445 | |
| Ile Gly Pro Ala Asn Gln Thr Leu Pro Lys Gly Ser Val Ala Thr Leu | | | |
| 450 | 455 | 460 | |
| Pro Cys Arg Ala Thr Gly Asn Pro Ser Pro Arg Ile Lys Trp Phe His | | | |
| 465 | 470 | 475 | 480 |
| Asp Gly His Ala Val Gln Ala Gly Asn Arg Tyr Ser Ile Ile Gln Gly | | | |
| 485 | 490 | 495 | |
| Ser Ser Leu Arg Val Asp Asp Leu Gln Leu Ser Asp Ser Gly Thr Tyr | | | |
| 500 | 505 | 510 | |
| Thr Cys Thr Ala Ser Gly Glu Arg Gly Glu Thr Ser Trp Ala Ala Thr | | | |
| 515 | 520 | 525 | |
| Leu Thr Val Glu Lys Pro Gly Ser Thr Ser Leu His Arg Ala Ala Asp | | | |
| 530 | 535 | 540 | |
| Pro Ser Thr Tyr Pro Ala Pro Pro Gly Thr Pro Lys Val Leu Asn Val | | | |
| 545 | 550 | 555 | 560 |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Arg | Thr | Ser | Ile | Ser | Leu | Arg | Trp | Ala | Lys | Ser | Gln | Glu | Lys | Pro | | | |
| | | | | | | | | | | | | | | | | 565 | 570 | 575 |
| Gly | Ala | Val | Gly | Pro | Ile | Ile | Gly | Tyr | Thr | Val | Glu | Tyr | Phe | Ser | Pro | | | |
| | | | | | | | | | | | | | | | | 580 | 585 | 590 |
| Asp | Leu | Gln | Thr | Gly | Trp | Ile | Val | Ala | Ala | His | Arg | Val | Gly | Asp | Thr | | | |
| | | | | | | | | | | | | | | | | 595 | 600 | 605 |
| Gln | Val | Thr | Ile | Ser | Gly | Leu | Thr | Pro | Gly | Thr | Ser | Tyr | Val | Phe | Leu | | | |
| | | | | | | | | | | | | | | | | 610 | 615 | 620 |
| Val | Arg | Ala | Glu | Asn | Thr | Gln | Gly | Ile | Ser | Val | Pro | Ser | Gly | Leu | Ser | | | |
| | | | | | | | | | | | | | | | | 625 | 630 | 635 |
| Asn | Val | Ile | Lys | Thr | Ile | Glu | Ala | Asp | Phe | Asp | Ala | Ala | Ser | Ala | Asn | | | |
| | | | | | | | | | | | | | | | | 645 | 650 | 655 |
| Asp | Leu | Ser | Ala | Ala | Arg | Thr | Leu | Leu | Thr | Gly | Lys | Ser | Val | Glu | Leu | | | |
| | | | | | | | | | | | | | | | | 660 | 665 | 670 |
| Ile | Asp | Ala | Ser | Ala | Ile | Asn | Ala | Ser | Ala | Val | Arg | Leu | Glu | Trp | Met | | | |
| | | | | | | | | | | | | | | | | 675 | 680 | 685 |
| Leu | His | Val | Ser | Ala | Asp | Glu | Lys | Tyr | Val | Glu | Gly | Leu | Arg | Ile | His | | | |
| | | | | | | | | | | | | | | | | 690 | 695 | 700 |
| Tyr | Lys | Asp | Ala | Ser | Val | Pro | Ser | Ala | Gln | Tyr | His | Ser | Ile | Thr | Val | | | |
| | | | | | | | | | | | | | | | | 705 | 710 | 715 |
| Met | Asp | Ala | Ser | Ala | Glu | Ser | Phe | Val | Val | Gly | Asn | Leu | Lys | Lys | Tyr | | | |
| | | | | | | | | | | | | | | | | 725 | 730 | 735 |
| Thr | Lys | Tyr | Glu | Phe | Phe | Leu | Thr | Pro | Phe | Phe | Glu | Thr | Ile | Glu | Gly | | | |
| | | | | | | | | | | | | | | | | 740 | 745 | 750 |
| Gln | Pro | Ser | Asn | Ser | Lys | Thr | Ala | Leu | Thr | Tyr | Glu | Asp | Val | Pro | Ser | | | |
| | | | | | | | | | | | | | | | | 755 | 760 | 765 |
| Ala | Pro | Pro | Asp | Asn | Ile | Gln | Ile | Gly | Met | Tyr | Asn | Gln | Thr | Ala | Gly | | | |
| | | | | | | | | | | | | | | | | 770 | 775 | 780 |
| Trp | Val | Arg | Trp | Thr | Pro | Pro | Pro | Ser | Gln | His | His | Asn | Gly | Asn | Leu | | | |
| | | | | | | | | | | | | | | | | 785 | 790 | 795 |
| Tyr | Gly | Tyr | Lys | Ile | Glu | Val | Ser | Ala | Gly | Asn | Thr | Met | Lys | Val | Leu | | | |
| | | | | | | | | | | | | | | | | 805 | 810 | 815 |
| Ala | Asn | Met | Thr | Leu | Asn | Ala | Thr | Thr | Thr | Ser | Val | Leu | Leu | Asn | Asn | | | |
| | | | | | | | | | | | | | | | | 820 | 825 | 830 |
| Leu | Thr | Thr | Gly | Ala | Val | Tyr | Ser | Val | Arg | Leu | Asn | Ser | Phe | Thr | Lys | | | |
| | | | | | | | | | | | | | | | | 835 | 840 | 845 |
| Ala | Gly | Asp | Gly | Pro | Tyr | Ser | Lys | Pro | Ile | Ser | Leu | Phe | Met | Asp | Pro | | | |
| | | | | | | | | | | | | | | | | 850 | 855 | 860 |

| | | | |
|---|------|------|------|
| Thr His His Val His Pro Pro Arg Ala His Pro Ser Gly Thr His Asp | | | |
| 865 | 870 | 875 | 880 |
| Gly Arg His Glu Gly Gln Asp Leu Thr Tyr His Asn Asn Gly Asn Ile | | | |
| | 885 | 890 | 895 |
| Pro Pro Gly Asp Ile Asn Pro Thr Thr His Lys Lys Thr Thr Asp Tyr | | | |
| | 900 | 905 | 910 |
| Leu Ser Gly Pro Trp Leu Met Val Leu Val Cys Ile Val Leu Leu Val | | | |
| | 915 | 920 | 925 |
| Leu Val Ile Ser Ala Ala Ile Ser Met Val Tyr Phe Lys Arg Lys His | | | |
| | 930 | 935 | 940 |
| Gln Met Thr Lys Glu Leu Gly His Leu Ser Val Val Ser Asp Asn Glu | | | |
| | 945 | 950 | 955 |
| Ile Thr Ala Leu Asn Ile Asn Ser Lys Glu Ser Leu Trp Ile Asp His | | | |
| | 965 | 970 | 975 |
| His Arg Gly Trp Arg Thr Ala Asp Thr Asp Lys Asp Ser Gly Leu Ser | | | |
| | 980 | 985 | 990 |
| Glu Ser Lys Leu Leu Ser His Val Asn Ser Ser Gln Ser Asn Tyr Asn | | | |
| | 995 | 1000 | 1005 |
| Asn Ser Asp Gly Gly Thr Asp Tyr Ala Glu Val Asp Thr Arg Asn Leu | | | |
| | 1010 | 1015 | 1020 |
| Thr Thr Phe Tyr Asn Cys Arg Lys Ser Pro Asp Asn Pro Thr Pro Tyr | | | |
| | 1025 | 1030 | 1035 |
| Ala Thr Thr Met Ile Ile Gly Thr Ser Ser Ser Glu Thr Cys Thr Lys | | | |
| | 1045 | 1050 | 1055 |
| Thr Thr Ser Ile Ser Ala Asp Lys Asp Ser Gly Thr His Ser Pro Tyr | | | |
| | 1060 | 1065 | 1070 |
| Ser Asp Ala Phe Ala Gly Gln Val Pro Ala Val Pro Val Val Lys Ser | | | |
| | 1075 | 1080 | 1085 |
| Asn Tyr Leu Gln Tyr Pro Val Glu Pro Ile Asn Trp Ser Glu Phe Leu | | | |
| | 1090 | 1095 | 1100 |
| Pro Pro Pro Pro Glu His Pro Pro Pro Ser Ser Thr Tyr Gly Tyr Ala | | | |
| 1105 | 1110 | 1115 | 1120 |
| Gln Gly Ser Pro Glu Ser Ser Arg Lys Ser Ser Lys Ser Ala Gly Ser | | | |
| | 1125 | 1130 | 1135 |
| Gly Ile Ser Thr Asn Gln Ser Ile Leu Asn Ala Ser Ile His Ser Ser | | | |
| | 1140 | 1145 | 1150 |
| Ser Ser Gly Gly Phe Ser Ala Trp Gly Val Ser Pro Gln Tyr Ala Val | | | |
| | 1155 | 1160 | 1165 |

Ala Cys Pro Pro Glu Asn Val Tyr Ser Asn Pro Leu Ser Ala Val Ala
 1170 1175 1180
 Gly Gly Thr Gln Asn Arg Tyr Gln Ile Thr Pro Thr Asn Gln His Pro
 1185 1190 1195 1200
 Pro Gln Leu Pro Ala Tyr Phe Ala Thr Thr Gly Pro Gly Gly Ala Val
 1205 1210 1215
 Pro Pro Asn His Leu Pro Phe Ala Thr Gln Arg His Ala Ala Ser Glu
 1220 1225 1230
 Tyr Gln Ala Gly Leu Asn Ala Ala Arg Cys Ala Gln Ser Arg Ala Cys
 1235 1240 1245
 Asn Ser Cys Asp Ala Leu Ala Thr Pro Ser Pro Met Gln Pro Pro Pro
 1250 1255 1260
 Pro Val Pro Val Pro Glu Gly Trp Tyr Gln Pro Val His Pro Asn Ser
 1265 1270 1275 1280
 His Pro Met His Pro Thr Ser Ser Asn His Gln Ile Tyr Gln Cys Ser
 1285 1290 1295
 Ser Glu Cys Ser Asp His Ser Arg Ser Ser Gln Ser His Lys Arg Gln
 1300 1305 1310
 Leu Gln Leu Glu Glu His Gly Ser Ser Ala Lys Gln Arg Gly Gly His
 1315 1320 1325
 His Arg Arg Arg Ala Pro Val Val Gln Pro Cys Met Glu Ser Glu Asn
 1330 1335 1340
 Glu Asn Met Leu Ala Glu Tyr Glu Gln Arg Gln Tyr Thr Ser Asp Cys
 1345 1350 1355 1360
 Cys Asn Ser Ser Arg Glu Gly Asp Thr Cys Ser Cys Ser Glu Gly Ser
 1365 1370 1375
 Cys Leu Tyr Ala Glu Ala Gly Glu Pro Ala Pro Arg Gln Met Thr Ala
 1380 1385 1390
 Lys Asn Thr
 1395

(2) INFORMATION FOR SEQ-ID-NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | | | | | | |
|------------|-------------|------------|-------------|------------|------------|------|
| GGTGAAAATC | CACGCATCAT | CGAGCATCCC | ATGGACACGA | CGGTGCCAAA | AAATGATCCA | 60 |
| TTTACGTTTA | ATTGCCAGGC | CGAGGGCAAT | CCAACACCAA | CCATTCAATG | GTTTAAGGAC | 120 |
| GGTCGCGAAC | TGAAGACGGA | TACGGGTTCG | CATCGCATAA | TGCTGCCCCG | CGGGGGTCTA | 180 |
| TTCTTTCTCA | AGGTTATCCA | CTCACGTAGA | GAGAGCGATG | CGGGCACTTA | CTGGTGCGAG | 240 |
| GCCAAAAACG | AGTTTGGAGT | GGCACGGTCC | AGGAATGCAA | CGTTGCAAGT | GGCAGTTCTC | 300 |
| CGCGACGAAT | TCCGTTTGGG | GCCGGCAAAT | ACCCGCGTGG | CCCAAGGCGA | GGTGGCCCTG | 360 |
| ATGGAATGCG | GTGCCCCCG | AGGATCTCCG | GAGCCGCAAA | TCTCGTGGCG | CAAGAACGGC | 420 |
| CAGACCCTGA | ATCTTGTCGG | GAACAAGCGG | ATTCGCATTG | TCGACGGTGG | CAATCTGGCC | 480 |
| ATCCAGGAAG | CCCGCCAATC | GGACGACGGA | CGCTACCAGT | GTGTGGTCAA | GAATGTGGTT | 540 |
| GGCACCCGGG | AGTCGGCCAC | CGCTTTTCTT | AAAGTGCATG | TACGTCCATT | CCTCATCCGA | 600 |
| GGACCCCA | ATCAGACGGC | GGTGGTGGGC | AGCTCGGTGG | TCTTCCAGTG | CCGCATCGGA | 660 |
| GGCGATCCCC | TGCCTGATGT | CCTGTGGCGA | CGCACTGCCT | CCGGCGGCAA | TATGCCACTG | 720 |
| CGTAAGTTTT | CTTGCTTCA | TTCAGCTTCA | GGTCGTGTGC | ACGTACTTGA | GGACCGCAGT | 780 |
| CTGAAGCTGG | ACGACGTTAC | TCTGGAGGAC | ATGGGCGAGT | ACACTTGCGA | GGCGGACAAT | 840 |
| GCGGTGGGCG | GCATCACGGC | CACTGGCATC | CTCACCGTTC | ACGCTCCCCC | CAAATTTGTG | 900 |
| ATACGCCCCA | AGAATCAGCT | GGTGGAGATC | GGTGATGAAG | TGCTGTTCGA | GTGCCAAGCG | 960 |
| AATGGACATC | CCCGACCAAC | GCTCTACTGG | TCGGTGGAGG | GCAACAGCTC | CCTGCTGCTC | 1020 |
| CCCGGCTATC | GGGATGGCCG | CATGGAAGTG | ACCCTGACGC | CCGAGGGGCG | CTCGGTGCTC | 1080 |
| TCGATAGCTC | GATTTGCCCG | TGAGGATTCC | GGAAAGGTGG | TCACTTGCAA | CGCCCTGAAC | 1140 |
| GCCGTGGGCA | GCGTCAGCAG | TCGGACTGTG | GTCAGTGTGG | ATACGCAATT | CGAGCTGCCA | 1200 |
| CCGCCGATTA | TCGAACAGGG | GCCCGTGAAT | CAAACGTTGC | CCGTTAAATC | AATTGTGGTT | 1260 |
| CTGCCATGCC | GAACCTCTGGG | CACTCCAGTG | CCACAGGTCT | CTTGGTACCT | GGATGGCATA | 1320 |
| CCCATCGATG | TGCAGGAGCA | CGAGCGGCGG | AATCTTTCGG | ACGCTGGAGC | CTTAACCATT | 1380 |
| TCGGATCTTC | AGCGCCACGA | GGATGAAGGC | TTGTACACCT | GCGTGGCCAG | CAATCGCAAC | 1440 |
| GGAAAATCCT | CTTGGAGTGG | TTACCTTCGT | CTGGACACCC | CGACAAATCC | GAATATCAAG | 1500 |
| TTCTTCAGAG | CCCCAGAACT | TTCCACCTAC | CCAGGGCCGC | CAGGAAAACC | GCAAATGGTG | 1560 |
| GAGAAGGGCG | AAAATTCGGT | GACTCTCAGC | TGGACGAGGA | GCAACAAGGT | GGGCGGCTCC | 1620 |
| AGTCTGGTGG | GCTATGTAAT | CGAGATGTTT | GGCAAAAACG | AAACGGATGG | CTGGGTGGCT | 1680 |
| GTGGGCACTA | GGGTGCAAAA | TACCACGTTT | ACCCAAACGG | GTCTGCTGCC | GGGTGTGAAT | 1740 |
| TACTTCTTTC | TAATTCGAGC | CGAGAACTCC | CATGGCTTAT | CACTGCCCAG | TCCGATGTGC | 1800 |
| GAACCCATTA | CGGTGGGAAC | GCGCTACTTC | AATAGTGGTC | TGGATCTGAG | CGAGGCTCGT | 1860 |
| GCCAGTCTGC | TGTCCGGAGA | TGTTGTGGAG | CTGAGCAACG | CCAGTGTGGT | GGACTCCACT | 1920 |
| AGCATGAAAC | TCACCTGGCA | GATCATCAAT | GGCAAAATACG | TCGAGGGCTT | CTATGTCTAT | 1980 |
| GCGAGACAGT | TGCCAAATCC | AATAGTCAAC | AATCCGGCGC | CCGTTACTAG | CAATACCAAT | 2040 |
| CCGCTGCTGG | GCTCTACATC | CACATCCGCA | TCCGCATCCG | CCTCGGCATC | GGCATTGATT | 2100 |
| TCGACAAAGC | CAAATATTGC | AGCTGCCGGC | AAACGTGATG | GGGAGACAAA | CCAGAGTGGA | 2160 |
| GGAGGAGCTC | CGACCCCACT | GAACACCAAG | TATCGCATGC | TAACGATTCT | CAATGGCGGT | 2220 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| GGCGCCTCAT | CCTGCACCAT | CACCGGGCTC | GTCCAGTACA | CGCTGTATGA | ATTTTTCATC | 2280 |
| GTGCCATTTT | ACAAATCCGT | CGAGGGCAAG | CCGTCGAATT | CGCGCATCGC | TCGCACCCTT | 2340 |
| GAAGATGTTT | CCTCTGAGGC | ACCATATGGA | ATGGAGGCTC | TGCTGTTGAA | CTCCTCCGCG | 2400 |
| GTCTTCCTCA | AATGGAAGGC | ACCAGAACTC | AAGGATCGGC | ATGGTGTTC | CTTGAACAT | 2460 |
| CATGTTATAG | TCCGAGGTAT | TGACACTGCC | CACAATTTCT | CACGCATTTT | GACAAATGTC | 2520 |
| ACCATCGATG | CCGCTTCGCC | TACTCTGGTT | TTGGCCAATC | TCACCGAAGG | CGTCATGTAC | 2580 |
| ACCGTGGGCG | TGGCGGCCGG | AAATAACGCT | GGAGTTGGTC | CTTATTGTGT | CCCAGCTACT | 2640 |
| TTGCGTTTGG | ATCCCATCAC | AAAGCGACTC | GATCCGTTCA | TCAATCAGCG | GGACCATGTT | 2700 |
| AACGATGTGC | TGACGCAGCC | CTGGTTCATA | ATACTCCTGG | GCGCCATCCT | GGCCGTTCTT | 2760 |
| ATGCTGTCCT | TTGGCGCAAT | GGTCTTTGTG | AAGCGCAAGC | ACATGATGAT | GAAGCAGTCG | 2820 |
| GCCCTAAATA | CAATGCGTGG | CAATCACACG | AGCGACGTGC | TCAAAATGCC | GAGTCTATCG | 2880 |
| GCGCGCAATG | GAAACGGCTA | CTGGCTGGAC | TCCTCCACCG | GCGGAATGGT | GTGGCGTCCC | 2940 |
| TCGCCCCGCG | GCGACTCGCT | GGAGATGCAA | AAGGATCACA | TCGCCGACTA | TGCGCCGGTC | 3000 |
| TGCGGTGCCC | CCGGTTCTCC | GGCCGGCGGT | GGCACCTCTT | CCGGTGGATC | CGGTGGCGCG | 3060 |
| GGCAGCGGTG | CCAGCGGCGG | CGATGACATT | CATGGAGGAC | ACGGCAGCGA | ACGCAATCAG | 3120 |
| CAGCGGTACG | TGGGCGAGTA | CTCCAACATA | CCGACCGACT | ATGCAGAGGT | GTCCAGTTTT | 3180 |
| GGCAAGGCAC | CCAGCGAGTA | TGGTCGGCAT | GGCAACGCCT | CCCCGGCCCC | TTATGCCACC | 3240 |
| TCTTCGATCC | TGAGTCCCCA | CCAGCAGCAA | CAGCAGCAGC | AGCCGCGTTA | TCAACAGCGA | 3300 |
| CCAGTGCCCC | GCTATGGGCT | CCAGCGCCCC | ATGCACCCAC | ACTACCAGCA | GCAGCAGCAT | 3360 |
| CAGCAGCAAC | AGGCGCAGCA | GACGCACCAG | CAACACCAGG | CTCTCCAGCA | GCACCAGCAA | 3420 |
| CTGCCACCCA | GCAACATCTA | CCAGCAGATG | TCCACCACCA | GCGAGATATA | CCCCACGAAC | 3480 |
| ACGGGTCCTT | CGCGCTCTGT | CTACTCTGAG | CAGTATTACT | ACCCCAAGGA | CAAGCAGAGA | 3540 |
| CACATCCACA | TCACCGAGAA | CAAGCTGAGC | AACTGCCACA | CCTATGAGGC | GGCTCCTGGC | 3600 |
| GCCAAGCAGT | CCTCGCCGAT | ATCCTCGCAG | TTCGCCAGCG | TGAGGCGGCA | GCAGCTGCCG | 3660 |
| CCCAACTGCA | GCATCGGCAG | GGAAAGTGCC | CGCTTCAAGG | TGCTAAACAC | GGATCAGGGC | 3720 |
| AAGAACCAGC | AGAATCTCCT | GGATCTCGAC | GGCTCCTCGA | TGTGCTACAA | CGGTCTGGCA | 3780 |
| GACTCGGGCT | GCGGTGGATC | TCCCTCCCCG | ATGGCCATGC | TGATGTCGCA | CGAGGACGAG | 3840 |
| CACGCGCTGT | ACCACACGGC | GGATGGGGAT | CTGGACGACA | TGGAACGACT | GTACGTCAAG | 3900 |
| GTGGACGAGC | AGCAGCCTCC | ACAGCAGCAG | CAGCAGCTGA | TTCCCCTGGT | CCCACAGCAT | 3960 |
| CCGGCGGAAG | GTCACCTGCA | GTCCTGGCGG | AATCAGAGCA | CGCGGAGCAG | TCGGAAGAAC | 4020 |
| GGCCAGGAAT | GCATCAAGGA | ACCCAGCGAG | TTGATCTACG | CTCCGGGAAG | CGTGGCCAGC | 4080 |
| GAACGGAGCC | TCCTCAGCAA | CTCGGGTAGC | GGCACCAGCA | GCCAGCCAGC | TGGCCACAAT | 4140 |
| GTCTGA | | | | | | 4146 |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1381 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Glu | Asn | Pro | Arg | Ile | Ile | Glu | His | Pro | Met | Asp | Thr | Thr | Val | Pro |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Lys | Asn | Asp | Pro | Phe | Thr | Phe | Asn | Cys | Gln | Ala | Glu | Gly | Asn | Pro | Thr |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Pro | Thr | Ile | Gln | Trp | Phe | Lys | Asp | Gly | Arg | Glu | Leu | Lys | Thr | Asp | Thr |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Gly | Ser | His | Arg | Ile | Met | Leu | Pro | Ala | Gly | Gly | Leu | Phe | Phe | Leu | Lys |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Val | Ile | His | Ser | Arg | Arg | Glu | Ser | Asp | Ala | Gly | Thr | Tyr | Trp | Cys | Glu |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Ala | Lys | Asn | Glu | Phe | Gly | Val | Ala | Arg | Ser | Arg | Asn | Ala | Thr | Leu | Gln |
| | | | 85 | | | | | 90 | | | | | 95 | | |
| Val | Ala | Val | Leu | Arg | Asp | Glu | Phe | Arg | Leu | Glu | Pro | Ala | Asn | Thr | Arg |
| | | 100 | | | | | | 105 | | | | | 110 | | |
| Val | Ala | Gln | Gly | Glu | Val | Ala | Leu | Met | Glu | Cys | Gly | Ala | Pro | Arg | Gly |
| | 115 | | | | | | 120 | | | | | 125 | | | |
| Ser | Pro | Glu | Pro | Gln | Ile | Ser | Trp | Arg | Lys | Asn | Gly | Gln | Thr | Leu | Asn |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Leu | Val | Gly | Asn | Lys | Arg | Ile | Arg | Ile | Val | Asp | Gly | Gly | Asn | Leu | Ala |
| 145 | | | | 150 | | | | | 155 | | | | | 160 | |
| Ile | Gln | Glu | Ala | Arg | Gln | Ser | Asp | Asp | Gly | Arg | Tyr | Gln | Cys | Val | Val |
| | | | 165 | | | | | 170 | | | | | 175 | | |
| Lys | Asn | Val | Val | Gly | Thr | Arg | Glu | Ser | Ala | Thr | Ala | Phe | Leu | Lys | Val |
| | | 180 | | | | | 185 | | | | | 190 | | | |
| His | Val | Arg | Pro | Phe | Leu | Ile | Arg | Gly | Pro | Gln | Asn | Gln | Thr | Ala | Val |
| | 195 | | | | | 200 | | | | | 205 | | | | |
| Val | Gly | Ser | Ser | Val | Val | Phe | Gln | Cys | Arg | Ile | Gly | Gly | Asp | Pro | Leu |
| | 210 | | | | | | 215 | | | | 220 | | | | |
| Pro | Asp | Val | Leu | Trp | Arg | Arg | Thr | Ala | Ser | Gly | Gly | Asn | Met | Pro | Leu |
| 225 | | | | 230 | | | | | 235 | | | | | 240 | |
| Arg | Lys | Phe | Ser | Trp | Leu | His | Ser | Ala | Ser | Gly | Arg | Val | His | Val | Leu |
| | | | 245 | | | | | 250 | | | | | 255 | | |
| Glu | Asp | Arg | Ser | Leu | Lys | Leu | Asp | Asp | Val | Thr | Leu | Glu | Asp | Met | Gly |
| | | 260 | | | | | 265 | | | | | 270 | | | |

| | | | |
|---|-----|-----|-----|
| Glu Tyr Thr Cys Glu Ala Asp Asn Ala Val Gly Gly Ile Thr Ala Thr | | | |
| 275 | 280 | 285 | |
| Gly Ile Leu Thr Val His Ala Pro Pro Lys Phe Val Ile Arg Pro Lys | | | |
| 290 | 295 | 300 | |
| Asn Gln Leu Val Glu Ile Gly Asp Glu Val Leu Phe Glu Cys Gln Ala | | | |
| 305 | 310 | 315 | 320 |
| Asn Gly His Pro Arg Pro Thr Leu Tyr Trp Ser Val Glu Gly Asn Ser | | | |
| | 325 | 330 | 335 |
| Ser Leu Leu Leu Pro Gly Tyr Arg Asp Gly Arg Met Glu Val Thr Leu | | | |
| | 340 | 345 | 350 |
| Thr Pro Glu Gly Arg Ser Val Leu Ser Ile Ala Arg Phe Ala Arg Glu | | | |
| | 355 | 360 | 365 |
| Asp Ser Gly Lys Val Val Thr Cys Asn Ala Leu Asn Ala Val Gly Ser | | | |
| | 370 | 375 | 380 |
| Val Ser Ser Arg Thr Val Val Ser Val Asp Thr Gln Phe Glu Leu Pro | | | |
| 385 | 390 | 395 | 400 |
| Pro Pro Ile Ile Glu Gln Gly Pro Val Asn Gln Thr Leu Pro Val Lys | | | |
| | 405 | 410 | 415 |
| Ser Ile Val Val Leu Pro Cys Arg Thr Leu Gly Thr Pro Val Pro Gln | | | |
| | 420 | 425 | 430 |
| Val Ser Trp Tyr Leu Asp Gly Ile Pro Ile Asp Val Gln Glu His Glu | | | |
| | 435 | 440 | 445 |
| Arg Arg Asn Leu Ser Asp Ala Gly Ala Leu Thr Ile Ser Asp Leu Gln | | | |
| | 450 | 455 | 460 |
| Arg His Glu Asp Glu Gly Leu Tyr Thr Cys Val Ala Ser Asn Arg Asn | | | |
| 465 | 470 | 475 | 480 |
| Gly Lys Ser Ser Trp Ser Gly Tyr Leu Arg Leu Asp Thr Pro Thr Asn | | | |
| | 485 | 490 | 495 |
| Pro Asn Ile Lys Phe Phe Arg Ala Pro Glu Leu Ser Thr Tyr Pro Gly | | | |
| | 500 | 505 | 510 |
| Pro Pro Gly Lys Pro Gln Met Val Glu Lys Gly Glu Asn Ser Val Thr | | | |
| | 515 | 520 | 525 |
| Leu Ser Trp Thr Arg Ser Asn Lys Val Gly Gly Ser Ser Leu Val Gly | | | |
| | 530 | 535 | 540 |
| Tyr Val Ile Glu Met Phe Gly Lys Asn Glu Thr Asp Gly Trp Val Ala | | | |
| 545 | 550 | 555 | 560 |
| Val Gly Thr Arg Val Gln Asn Thr Thr Phe Thr Gln Thr Gly Leu Leu | | | |
| | 565 | 570 | 575 |

Pro Gly Val Asn Tyr Phe Phe Leu Ile Arg Ala Glu Asn Ser His Gly
 580 585 590
 Leu Ser Leu Pro Ser Pro Met Ser Glu Pro Ile Thr Val Gly Thr Arg
 595 600 605
 Tyr Phe Asn Ser Gly Leu Asp Leu Ser Glu Ala Arg Ala Ser Leu Leu
 610 615 620
 Ser Gly Asp Val Val Glu Leu Ser Asn Ala Ser Val Val Asp Ser Thr
 625 630 635 640
 Ser Met Lys Leu Thr Trp Gln Ile Ile Asn Gly Lys Tyr Val Glu Gly
 645 650 655
 Phe Tyr Val Tyr Ala Arg Gln Leu Pro Asn Pro Ile Val Asn Asn Pro
 660 665 670
 Ala Pro Val Thr Ser Asn Thr Asn Pro Leu Leu Gly Ser Thr Ser Thr
 675 680 685
 Ser Ala Ser Ala Ser Ala Ser Ala Ser Ala Leu Ile Ser Thr Lys Pro
 690 695 700
 Asn Ile Ala Ala Ala Gly Lys Arg Asp Gly Glu Thr Asn Gln Ser Gly
 705 710 715 720
 Gly Gly Ala Pro Thr Pro Leu Asn Thr Lys Tyr Arg Met Leu Thr Ile
 725 730 735
 Leu Asn Gly Gly Gly Ala Ser Ser Cys Thr Ile Thr Gly Leu Val Gln
 740 745 750
 Tyr Thr Leu Tyr Glu Phe Phe Ile Val Pro Phe Tyr Lys Ser Val Glu
 755 760 765
 Gly Lys Pro Ser Asn Ser Arg Ile Ala Arg Thr Leu Glu Asp Val Pro
 770 775 780
 Ser Glu Ala Pro Tyr Gly Met Glu Ala Leu Leu Leu Asn Ser Ser Ala
 785 790 795 800
 Val Phe Leu Lys Trp Lys Ala Pro Glu Leu Lys Asp Arg His Gly Val
 805 810 815
 Leu Leu Asn Tyr His Val Ile Val Arg Gly Ile Asp Thr Ala His Asn
 820 825 830
 Phe Ser Arg Ile Leu Thr Asn Val Thr Ile Asp Ala Ala Ser Pro Thr
 835 840 845
 Leu Val Leu Ala Asn Leu Thr Glu Gly Val Met Tyr Thr Val Gly Val
 850 855 860
 Ala Ala Gly Asn Asn Ala Gly Val Gly Pro Tyr Cys Val Pro Ala Thr
 865 870 875 880

| | | | |
|---|------|------|------|
| Leu Arg Leu Asp Pro Ile Thr Lys Arg Leu Asp Pro Phe Ile Asn Gln | | | |
| | 885 | 890 | 895 |
| Arg Asp His Val Asn Asp Val Leu Thr Gln Pro Trp Phe Ile Ile Leu | | | |
| | 900 | 905 | 910 |
| Leu Gly Ala Ile Leu Ala Val Leu Met Leu Ser Phe Gly Ala Met Val | | | |
| | 915 | 920 | 925 |
| Phe Val Lys Arg Lys His Met Met Met Lys Gln Ser Ala Leu Asn Thr | | | |
| | 930 | 935 | 940 |
| Met Arg Gly Asn His Thr Ser Asp Val Leu Lys Met Pro Ser Leu Ser | | | |
| | 945 | 950 | 955 |
| Ala Arg Asn Gly Asn Gly Tyr Trp Leu Asp Ser Ser Thr Gly Gly Met | | | |
| | 965 | 970 | 975 |
| Val Trp Arg Pro Ser Pro Gly Gly Asp Ser Leu Glu Met Gln Lys Asp | | | |
| | 980 | 985 | 990 |
| His Ile Ala Asp Tyr Ala Pro Val Cys Gly Ala Pro Gly Ser Pro Ala | | | |
| | 995 | 1000 | 1005 |
| Gly Gly Gly Thr Ser Ser Gly Gly Ser Gly Gly Ala Gly Ser Gly Ala | | | |
| | 1010 | 1015 | 1020 |
| Ser Gly Gly Asp Asp Ile His Gly Gly His Gly Ser Glu Arg Asn Gln | | | |
| | 1025 | 1030 | 1035 |
| Gln Arg Tyr Val Gly Glu Tyr Ser Asn Ile Pro Thr Asp Tyr Ala Glu | | | |
| | 1045 | 1050 | 1055 |
| Val Ser Ser Phe Gly Lys Ala Pro Ser Glu Tyr Gly Arg His Gly Asn | | | |
| | 1060 | 1065 | 1070 |
| Ala Ser Pro Ala Pro Tyr Ala Thr Ser Ser Ile Leu Ser Pro His Gln | | | |
| | 1075 | 1080 | 1085 |
| Gln Gln Gln Gln Gln Gln Pro Arg Tyr Gln Gln Arg Pro Val Pro Gly | | | |
| | 1090 | 1095 | 1100 |
| Tyr Gly Leu Gln Arg Pro Met His Pro His Tyr Gln Gln Gln Gln His | | | |
| | 1105 | 1110 | 1115 |
| Gln Gln Gln Gln Ala Gln Gln Thr His Gln Gln His Gln Ala Leu Gln | | | |
| | 1125 | 1130 | 1135 |
| Gln His Gln Gln Leu Pro Pro Ser Asn Ile Tyr Gln Gln Met Ser Thr | | | |
| | 1140 | 1145 | 1150 |
| Thr Ser Glu Ile Tyr Pro Thr Asn Thr Gly Pro Ser Arg Ser Val Tyr | | | |
| | 1155 | 1160 | 1165 |
| Ser Glu Gln Tyr Tyr Tyr Pro Lys Asp Lys Gln Arg His Ile His Ile | | | |
| | 1170 | 1175 | 1180 |

| | | | |
|---|------|------|------|
| Thr Glu Asn Lys Leu Ser Asn Cys His Thr Tyr Glu Ala Ala Pro Gly | | | |
| 1185 | 1190 | 1195 | 1200 |
| Ala Lys Gln Ser Ser Pro Ile Ser Ser Gln Phe Ala Ser Val Arg Arg | | | |
| | 1205 | 1210 | 1215 |
| Gln Gln Leu Pro Pro Asn Cys Ser Ile Gly Arg Glu Ser Ala Arg Phe | | | |
| | 1220 | 1225 | 1230 |
| Lys Val Leu Asn Thr Asp Gln Gly Lys Asn Gln Gln Asn Leu Leu Asp | | | |
| | 1235 | 1240 | 1245 |
| Leu Asp Gly Ser Ser Met Cys Tyr Asn Gly Leu Ala Asp Ser Gly Cys | | | |
| | 1250 | 1255 | 1260 |
| Gly Gly Ser Pro Ser Pro Met Ala Met Leu Met Ser His Glu Asp Glu | | | |
| 1265 | 1270 | 1275 | 1280 |
| His Ala Leu Tyr His Thr Ala Asp Gly Asp Leu Asp Asp Met Glu Arg | | | |
| | 1285 | 1290 | 1295 |
| Leu Tyr Val Lys Val Asp Glu Gln Gln Pro Pro Gln Gln Gln Gln Gln | | | |
| | 1300 | 1305 | 1310 |
| Leu Ile Pro Leu Val Pro Gln His Pro Ala Glu Gly His Leu Gln Ser | | | |
| | 1315 | 1320 | 1325 |
| Trp Arg Asn Gln Ser Thr Arg Ser Ser Arg Lys Asn Gly Gln Glu Cys | | | |
| | 1330 | 1335 | 1340 |
| Ile Lys Glu Pro Ser Glu Leu Ile Tyr Ala Pro Gly Ser Val Ala Ser | | | |
| 1345 | 1350 | 1355 | 1360 |
| Glu Arg Ser Leu Leu Ser Asn Ser Gly Ser Gly Thr Ser Ser Gln Pro | | | |
| | 1365 | 1370 | 1375 |
| Ala Gly His Asn Val | | | |
| | 1380 | | |

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | |
|---|-----|
| ATGTACTATC TAGGTTTTTA CCACACTCAC ACACACACAC ACACATACAT AAATTTTGAT | 60 |
| AAAATTCCTA ATGCCTCAAA TCTCGCTCCC GTGATAATCG AACATCCCAT CGATGTGGTG | 120 |
| GTATCTAGGG GATCGCCAGC AACCTCAAC TGTGGTGCAA AGCCATCTAC CGCCAAAATC | 180 |

| | | | | | | |
|-------------|------------|------------|------------|------------|-------------|------|
| ACATGGTACA | AGGATGGACA | GCCCGTAATC | ACGAATAAGG | AGCAAGTGAA | CAGCCACCGG | 240 |
| ATTGTTCTCG | ACACGGGATC | CCTGTTTCTT | CTGAAAGTGA | ATAGTGGAAA | AAACGGAAAA | 300 |
| GACAGCGATG | CGGGAGCGTA | CTATTGTGTG | GCCAGCAACG | AGCACGGAGA | AGTGAAGTCG | 360 |
| AACGAAGGAT | CGTTAAAT | GGCGATGCTT | CGCGAAGACT | TTCGAGTTCG | GCCAAGAACA | 420 |
| GTTTCAGGCTC | TTGGTGGAGA | GATGGCCGTT | CTGGAATGCA | GTCCGCCACG | TGGATTCCCCG | 480 |
| GAGCCGGTTG | TGAGCTGGCG | GAAAGACGAC | AAAGAGCTCC | GAATTCAAGA | CATGCCACGA | 540 |
| TACACTCTAC | ACTCTGACGG | AAACCTCATC | ATTGATCCGG | TCGATCGAAG | CGATTCTGGT | 600 |
| ACTTATCAGT | GTGTTGCCAA | CAACATGGTC | GGAGAACGGG | TGTCCAATCC | CGCAAGATTG | 660 |
| AGTGTCTTTG | AGAAACCAAA | GTTTGAGCAA | GAACCCAAGG | ACATGACGGT | CGACGTCGGA | 720 |
| GCCGCAGTGC | TGTTTGATTG | TCGTGTGACT | GGAGATCCTC | AACCACAAAT | TACGTGGAAA | 780 |
| CGCAAAAATG | AGCCGATGCC | AGTTACACGT | GCATACATTG | CCAAGGATAA | TCGGGGGTTG | 840 |
| AGAATCGAAA | GAGTTCAACC | ATCAGACGAA | GGTGAATACG | TTTGCTATGC | ACGAAATCCA | 900 |
| GCGGGAACTC | TTGAAGCATC | TGCACATCTT | CGTGTCCAGG | CACCTCCATC | CTTCCAGACA | 960 |
| AAACCAGCAG | ACCAGTCAGT | TCCAGCTGGA | GGCACGGCAA | CTTTTGAATG | CACCTTGGTC | 1020 |
| GGTCAACCGA | GTCCCGCCTA | TTTTTGGAGC | AAGGAAGGCC | AACAGGATCT | TCTTTTCCCA | 1080 |
| AGTTATGTGT | CCGCTGATGG | TAGAACGAAA | GTTTCACCAA | CTGGAACATT | GACAATTGAG | 1140 |
| GAAGTTCGTC | AAGTTGATGA | GGGAGCTTAT | GTGTGCGCTG | GAATGAACTC | GGCAGGAAGC | 1200 |
| TCGTTGAGCA | AGGCAGCTTT | GAAAGCAACA | TTTGAAACCA | AAGGCCGTGT | CCAAAAA | 1260 |
| AAGAGCAAAA | TGGGCAAACA | GAAACAAAAA | AATGTTCAAT | CAATTATCAA | ATATTTAATT | 1320 |
| TCAGCCGTGA | CCGGAAACAC | ACCCGCCAAA | CCACCACCAA | CAATCGAGCA | TGGTCATCAA | 1380 |
| AATCAGACCC | TTATGGTTGG | ATCATCAGCC | ATCCTTCCAT | GTCAGGCTAG | CGGAAAACCA | 1440 |
| ACTCCAGGAA | TATCATGGCT | CAGGGATGGG | CTACCTATTG | ACATTACAGA | TAGTCGTATC | 1500 |
| AGTCAACATT | CAACGGGAAG | TCTACATATT | GCCGATTTAA | AGAAACCTGA | CACCGGAGTT | 1560 |
| TACACTTGCA | TTGCGAAGAA | CGAGGATGGA | GAGTCAACAT | GGTCGGCATC | TCTGACTGTT | 1620 |
| GAAGATCACA | CTAGCAATGC | ACAATTTGTT | CGGATGCCGG | ATCCATCGAA | CTTCCCGTCT | 1680 |
| TCTCCAACGC | AACCCATTAT | TGTCAATGTC | ACTGATACCG | AAGTAGAGCT | CCACTGGAAT | 1740 |
| GCTCCCTCCA | CATCTGGCGC | AGGACCAATC | ACTGGTTATA | TCATTAGTA | CTACAGTCCA | 1800 |
| GACCTCGGAC | AGACGTGGTT | TAACATTCCA | GACTACGTGG | CATCTACTGA | ATATAGAATA | 1860 |
| AAGGGTCTGA | AACCATCTCA | CTCGTATATG | TTTGTGATTC | GAGCAGAAAA | TGAGAAAGGT | 1920 |
| ATTGGAACGC | CGAGTGTGTC | GTCGGCTCTC | GTTACCACTA | GCAAGCCAGC | AGCTCAAGTT | 1980 |
| GCGCTTTCTG | ACAAGAACAA | AATGGACATG | GCCATCGCTG | AGAAGAGACT | CACTTCGGAA | 2040 |
| CAACTCATAA | AACCTGAGGA | AGTGAAGACT | ATTAATTCTA | CGGCCGTTCG | TTTGTTCTGG | 2100 |
| AAGAAGAGGA | AACCTGAAGA | GCTGATTGAT | GGTACTACA | TCAAGTGGAG | AGGGCCTCCA | 2160 |
| AGAACCAATG | ATAATCAATA | CGTGAATGTG | ACCAGCCCTA | GCACCGAAAA | CTATGTTGTT | 2220 |
| TCAAATTTAA | TGCCATTAC | CAACTATGAG | TTTTTCGTGA | TTCTTATCA | TTCCGGAGTT | 2280 |
| CATAGTATTC | ATGGAGCACC | GAGTAATTCC | ATGGACGTGT | TGACCGCCGA | AGCTCCACCT | 2340 |
| TCATTGCCAC | CAGAGGATGT | GCGAATCCGT | ATGCTCAACC | TGACCACTCT | TCGTATCTCT | 2400 |
| TGGAAAGCAC | CAAAAGCCGA | CGGCATCAAC | GGAATTCTCA | AAGGATTCCA | AATTGTTATT | 2460 |

| | | | | | | |
|-------------|-------------|------------|-------------|------------|------------|------|
| GTTGGTCAAG | CGCCCAACAA | CAATCGGAAC | ATCACTACAA | ACGAGAGAGC | TGCCAGTGTT | 2520 |
| ACTCTGTTCC | ATTTAGTGAC | TGGAATGACG | TATAAAATTC | GTGTAGCGGC | TAGAAGCAAT | 2580 |
| GGTGGAGTTG | GAGTCTCACA | TGGAACGAGT | GAAAGTCATCA | TGAATCAAGA | CACGCTGGAA | 2640 |
| AAACACCTTG | CTGCTCAACA | AGAAAACGAA | TCATTTTTGT | ATGGGCTGAT | CAATAAATCT | 2700 |
| CATGTTCCCTG | TGATTGTCAT | TGTTGCAATT | CTGATTATTT | TCGTAGTCAT | CATTATAGCC | 2760 |
| TATTGTTACT | GGAGGAATAG | CAGAAACAGT | GATGGAAAGG | ATCGAAGTTT | TATAAAGATC | 2820 |
| AATGATGGAA | GTGTTTCATAT | GGCTTCGAAT | AATCTTTGGG | ATGTTGCACA | AAATCCGAAT | 2880 |
| CAGAATCCAA | TGTACAACAC | TGCTGGAAGA | ATGACTATGA | ACAATAGAAA | TGGCCAGGCT | 2940 |
| CTCTATTTCGC | TGACACCAAA | TGCGCAAGAC | TTTTTCAACA | ATTGTGATGA | CTACAGTGGA | 3000 |
| ACGATGCACA | GACCAGGATC | CGAGCATCAC | TATCATTATG | CTCAACTGAC | TGGCGGACCT | 3060 |
| GGTAATGCGA | TGTCTACTTT | TTATGGAAAC | CAATATCACG | ATGATCCATC | TCCATATGCC | 3120 |
| ACCACAACAC | TGGTCCTGTC | GAACCAACAA | CCAGCTTGGC | TCAATGACAA | AATGCTTCGC | 3180 |
| GCGCCAGCAA | TGCCAACAAA | TCCCGTGCCA | CCAGAGCCAC | CGGCGCGATA | TGCAGATCAT | 3240 |
| ACCGCTGGAA | GACGATCTCG | ATCGAGCCGT | GCATCCGATG | GGAGAGGAAC | TCTGAATGGC | 3300 |
| GGACTCCATC | ACCGGACTAG | CGGAAGTCAA | CGGTCGGATA | GTCCACCTCA | CACAGATGTG | 3360 |
| AGCTATGTTT | AGCTTCACTC | ATCCGATGGA | ACTGGTAGTA | GTAAGGAAAG | AACTGGGGAG | 3420 |
| CGGAGAACAC | CACCGAATAA | GACTCTGATG | GACTTTATTC | CGCCACCACC | TTCCAATCCA | 3480 |
| CCACCACCTG | GAGGGCACGT | TTATGACACA | GCAACTAGGC | GTCAGTTGAA | TCGTGGAAGT | 3540 |
| ACTCCACGAG | AAGACACCTA | CGATTCCGGT | AGTGACGGAG | CTTTTGCTCG | GGTTGATGTG | 3600 |
| AATGCAAGGC | CAACGAGTCG | GAATCGGAAT | TTGGGAGGAA | GGCCGCTGAA | AGGGAAACGA | 3660 |
| GACGACGATA | GTCAGCGGTC | TTCGTTGATG | ATGGACGATG | ATGGTGGATC | TTCTGAAGCT | 3720 |
| GACGGGGAGA | ACTCTGAAGG | AGACGTTCCG | CGTGGAGGTG | TTAGAAAAGC | AGTTCCTCGA | 3780 |
| ATGGGTATCT | CTGCAAGTAC | GCTGGCTCAT | AGTTGTTACG | GGACAAACGG | CACTGCTCAA | 3840 |
| CGATTCCGGT | CAATTCCACG | TAACAATGGA | ATCGTCACAC | AAGAACAAAC | TTGA | 3894 |

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1297 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

| | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Tyr | Tyr | Leu | Gly | Phe | Tyr | His | Thr | His | Thr | His | Thr | Tyr |
| 1 | | | 5 | | | | | 10 | | | | 15 | |
| Ile | Asn | Phe | Asp | Lys | Ile | Pro | Asn | Ala | Ser | Asn | Leu | Ala | Pro |
| | | | 20 | | | | | 25 | | | | 30 | |
| Ile | Glu | His | Pro | Ile | Asp | Val | Val | Val | Ser | Arg | Gly | Ser | Pro |
| | | | | | | | | | | | | | Thr |

| | | |
|---|-----|-----|
| 35 | 40 | 45 |
| Leu Asn Cys Gly Ala Lys Pro Ser Thr Ala Lys Ile Thr Trp Tyr Lys | | |
| 50 | 55 | 60 |
| Asp Gly Gln Pro Val Ile Thr Asn Lys Glu Gln Val Asn Ser His Arg | | |
| 65 | 70 | 75 |
| Ile Val Leu Asp Thr Gly Ser Leu Phe Leu Leu Lys Val Asn Ser Gly | | |
| 85 | 90 | 95 |
| Lys Asn Gly Lys Asp Ser Asp Ala Gly Ala Tyr Tyr Cys Val Ala Ser | | |
| 100 | 105 | 110 |
| Asn Glu His Gly Glu Val Lys Ser Asn Glu Gly Ser Leu Lys Leu Ala | | |
| 115 | 120 | 125 |
| Met Leu Arg Glu Asp Phe Arg Val Arg Pro Arg Thr Val Gln Ala Leu | | |
| 130 | 135 | 140 |
| Gly Gly Glu Met Ala Val Leu Glu Cys Ser Pro Pro Arg Gly Phe Pro | | |
| 145 | 150 | 155 |
| Glu Pro Val Val Ser Trp Arg Lys Asp Asp Lys Glu Leu Arg Ile Gln | | |
| 165 | 170 | 175 |
| Asp Met Pro Arg Tyr Thr Leu His Ser Asp Gly Asn Leu Ile Ile Asp | | |
| 180 | 185 | 190 |
| Pro Val Asp Arg Ser Asp Ser Gly Thr Tyr Gln Cys Val Ala Asn Asn | | |
| 195 | 200 | 205 |
| Met Val Gly Glu Arg Val Ser Asn Pro Ala Arg Leu Ser Val Phe Glu | | |
| 210 | 215 | 220 |
| Lys Pro Lys Phe Glu Gln Glu Pro Lys Asp Met Thr Val Asp Val Gly | | |
| 225 | 230 | 235 |
| Ala Ala Val Leu Phe Asp Cys Arg Val Thr Gly Asp Pro Gln Pro Gln | | |
| 245 | 250 | 255 |
| Ile Thr Trp Lys Arg Lys Asn Glu Pro Met Pro Val Thr Arg Ala Tyr | | |
| 260 | 265 | 270 |
| Ile Ala Lys Asp Asn Arg Gly Leu Arg Ile Glu Arg Val Gln Pro Ser | | |
| 275 | 280 | 285 |
| Asp Glu Gly Glu Tyr Val Cys Tyr Ala Arg Asn Pro Ala Gly Thr Leu | | |
| 290 | 295 | 300 |
| Glu Ala Ser Ala His Leu Arg Val Gln Ala Pro Pro Ser Phe Gln Thr | | |
| 305 | 310 | 315 |
| Lys Pro Ala Asp Gln Ser Val Pro Ala Gly Gly Thr Ala Thr Phe Glu | | |
| 325 | 330 | 335 |
| Cys Thr Leu Val Gly Gln Pro Ser Pro Ala Tyr Phe Trp Ser Lys Glu | | |

B98-006

| 645 | | | | | 650 | | | | | 655 | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ala | Ala | Gln | Val | Ala | Leu | Ser | Asp | Lys | Asn | Lys | Met | Asp | Met | Ala | Ile | |
| 660 | | | | | 665 | | | | | 670 | | | | | | |
| Ala | Glu | Lys | Arg | Leu | Thr | Ser | Glu | Gln | Leu | Ile | Lys | Leu | Glu | Glu | Val | |
| 675 | | | | | 680 | | | | | 685 | | | | | | |
| Lys | Thr | Ile | Asn | Ser | Thr | Ala | Val | Arg | Leu | Phe | Trp | Lys | Lys | Arg | Lys | |
| 690 | | | | | 695 | | | | | 700 | | | | | | |
| Leu | Glu | Glu | Leu | Ile | Asp | Gly | Tyr | Tyr | Ile | Lys | Trp | Arg | Gly | Pro | Pro | |
| 705 | | | | | 710 | | | | | 715 | | | | | 720 | |
| Arg | Thr | Asn | Asp | Asn | Gln | Tyr | Val | Asn | Val | Thr | Ser | Pro | Ser | Thr | Glu | |
| 725 | | | | | 730 | | | | | 735 | | | | | | |
| Asn | Tyr | Val | Val | Ser | Asn | Leu | Met | Pro | Phe | Thr | Asn | Tyr | Glu | Phe | Phe | |
| 740 | | | | | 745 | | | | | 750 | | | | | | |
| Val | Ile | Pro | Tyr | His | Ser | Gly | Val | His | Ser | Ile | His | Gly | Ala | Pro | Ser | |
| 755 | | | | | 760 | | | | | 765 | | | | | | |
| Asn | Ser | Met | Asp | Val | Leu | Thr | Ala | Glu | Ala | Pro | Pro | Ser | Leu | Pro | Pro | |
| 770 | | | | | 775 | | | | | 780 | | | | | | |
| Glu | Asp | Val | Arg | Ile | Arg | Met | Leu | Asn | Leu | Thr | Thr | Leu | Arg | Ile | Ser | |
| 785 | | | | | 790 | | | | | 795 | | | | | 800 | |
| Trp | Lys | Ala | Pro | Lys | Ala | Asp | Gly | Ile | Asn | Gly | Ile | Leu | Lys | Gly | Phe | |
| 805 | | | | | 810 | | | | | 815 | | | | | | |
| Gln | Ile | Val | Ile | Val | Gly | Gln | Ala | Pro | Asn | Asn | Asn | Arg | Asn | Ile | Thr | |
| 820 | | | | | 825 | | | | | 830 | | | | | | |
| Thr | Asn | Glu | Arg | Ala | Ala | Ser | Val | Thr | Leu | Phe | His | Leu | Val | Thr | Gly | |
| 835 | | | | | 840 | | | | | 845 | | | | | | |
| Met | Thr | Tyr | Lys | Ile | Arg | Val | Ala | Ala | Arg | Ser | Asn | Gly | Gly | Val | Gly | |
| 850 | | | | | 855 | | | | | 860 | | | | | | |
| Val | Ser | His | Gly | Thr | Ser | Glu | Val | Ile | Met | Asn | Gln | Asp | Thr | Leu | Glu | |
| 865 | | | | | 870 | | | | | 875 | | | | | 880 | |
| Lys | His | Leu | Ala | Ala | Gln | Gln | Glu | Asn | Glu | Ser | Phe | Leu | Tyr | Gly | Leu | |
| 885 | | | | | 890 | | | | | 895 | | | | | | |
| Ile | Asn | Lys | Ser | His | Val | Pro | Val | Ile | Val | Ile | Val | Ala | Ile | Leu | Ile | |
| 900 | | | | | 905 | | | | | 910 | | | | | | |
| Ile | Phe | Val | Val | Ile | Ile | Ile | Ala | Tyr | Cys | Tyr | Trp | Arg | Asn | Ser | Arg | |
| 915 | | | | | 920 | | | | | 925 | | | | | | |
| Asn | Ser | Asp | Gly | Lys | Asp | Arg | Ser | Phe | Ile | Lys | Ile | Asn | Asp | Gly | Ser | |
| 930 | | | | | 935 | | | | | 940 | | | | | | |
| Val | His | Met | Ala | Ser | Asn | Asn | Leu | Trp | Asp | Val | Ala | Gln | Asn | Pro | Asn | |

| | | | |
|---|------|------|------|
| 945 | 950 | 955 | 960 |
| Gln Asn Pro Met Tyr Asn Thr Ala Gly Arg Met Thr Met Asn Asn Arg | | | |
| | 965 | 970 | 975 |
| Asn Gly Gln Ala Leu Tyr Ser Leu Thr Pro Asn Ala Gln Asp Phe Phe | | | |
| | 980 | 985 | 990 |
| Asn Asn Cys Asp Asp Tyr Ser Gly Thr Met His Arg Pro Gly Ser Glu | | | |
| | 995 | 1000 | 1005 |
| His His Tyr His Tyr Ala Gln Leu Thr Gly Gly Pro Gly Asn Ala Met | | | |
| | 1010 | 1015 | 1020 |
| Ser Thr Phe Tyr Gly Asn Gln Tyr His Asp Asp Pro Ser Pro Tyr Ala | | | |
| 1025 | 1030 | 1035 | 1040 |
| Thr Thr Thr Leu Val Leu Ser Asn Gln Gln Pro Ala Trp Leu Asn Asp | | | |
| | 1045 | 1050 | 1055 |
| Lys Met Leu Arg Ala Pro Ala Met Pro Thr Asn Pro Val Pro Pro Glu | | | |
| | 1060 | 1065 | 1070 |
| Pro Pro Ala Arg Tyr Ala Asp His Thr Ala Gly Arg Arg Ser Arg Ser | | | |
| | 1075 | 1080 | 1085 |
| Ser Arg Ala Ser Asp Gly Arg Gly Thr Leu Asn Gly Gly Leu His His | | | |
| | 1090 | 1095 | 1100 |
| Arg Thr Ser Gly Ser Gln Arg Ser Asp Ser Pro Pro His Thr Asp Val | | | |
| 1105 | 1110 | 1115 | 1120 |
| Ser Tyr Val Gln Leu His Ser Ser Asp Gly Thr Gly Ser Ser Lys Glu | | | |
| | 1125 | 1130 | 1135 |
| Arg Thr Gly Glu Arg Arg Thr Pro Pro Asn Lys Thr Leu Met Asp Phe | | | |
| | 1140 | 1145 | 1150 |
| Ile Pro Pro Pro Pro Ser Asn Pro Pro Pro Pro Gly Gly His Val Tyr | | | |
| | 1155 | 1160 | 1165 |
| Asp Thr Ala Thr Arg Arg Gln Leu Asn Arg Gly Ser Thr Pro Arg Glu | | | |
| | 1170 | 1175 | 1180 |
| Asp Thr Tyr Asp Ser Val Ser Asp Gly Ala Phe Ala Arg Val Asp Val | | | |
| 1185 | 1190 | 1195 | 1200 |
| Asn Ala Arg Pro Thr Ser Arg Asn Arg Asn Leu Gly Gly Arg Pro Leu | | | |
| | 1205 | 1210 | 1215 |
| Lys Gly Lys Arg Asp Asp Asp Ser Gln Arg Ser Ser Leu Met Met Asp | | | |
| | 1220 | 1225 | 1230 |
| Asp Asp Gly Gly Ser Ser Glu Ala Asp Gly Glu Asn Ser Glu Gly Asp | | | |
| | 1235 | 1240 | 1245 |
| Val Pro Arg Gly Gly Val Arg Lys Ala Val Pro Arg Met Gly Ile Ser | | | |

| | | | |
|---|------|------|------|
| 1250 | 1255 | 1260 | |
| Ala Ser Thr Leu Ala His Ser Cys Tyr Gly Thr Asn Gly Thr Ala Gln | | | |
| 1265 | 1270 | 1275 | 1280 |
| Arg Phe Arg Ser Ile Pro Arg Asn Asn Gly Ile Val Thr Gln Glu Gln | | | |
| | 1285 | 1290 | 1295 |
| Thr | | | |

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4956 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| | |
|--|------|
| ATGAAATGGA AACATGTTCC TTTTTTGGTC ATGATATCAC TCCTCAGCTT ATCCCCAAAT | 60 |
| CACCTGTTTC TGGCCCAGCT TATTCCAGAC CCTGAAGATG TAGAGAGGGG GAACGACCAC | 120 |
| GGGACGCCAA TCCCCACCTC TGATAACGAT GACAATTCGC TGGGCTATAC AGGCTCCCGT | 180 |
| CTTCGTCAGG AAGATTTTCC ACCTCGCATT GTTGAACACC CTTCAGACCT GATTGTCTCA | 240 |
| AAAGGAGAAC CTGCAACTTT GAACTGCAAA GCTGAAGGCC GCCCCACACC CACTATTGAA | 300 |
| TGGTACAAAG GGGGAGAGAG AGTGGAGACA GACAAAGATG ACCCTCGCTC ACACCGAATG | 360 |
| TTGCTGCCGA GTGGATCTTT ATTTTCTTA CGTATAGTAC ATGGACGGAA AAGTAGACCT | 420 |
| GATGAAGGAG TCTATGTCTG TGTAAGCAAGG AATTACCTTG GAGAGGCTGT GAGCCACAAT | 480 |
| GCATCGCTGG AAGTAGCCAT ACTTCGGGAT GACTTCAGAC AAAACCCTTC GGATGTCATG | 540 |
| GTTGCAGTAG GAGAGCCTGC AGTAATGGAA TGCCAACCTC CACGAGGCCA TCCTGAGCCC | 600 |
| ACCATTTTCAT GGAAGAAAGA TGGCTCTCCA CTGGATGATA AAGATGAAAG AATAACTATA | 660 |
| CGAGGAGGAA AGCTCATGAT CACTTACACC CGTAAAAGTG ACGCTGGCAA ATATGTTTGT | 720 |
| GTTGGTACCA ATATGGTTGG GGAACGTGAG AGTGAAGTAG CCGAGCTGAC TGTCTTAGAG | 780 |
| AGACCATCAT TTGTGAAGAG ACCCAGTAAC TTGGCAGTAA CTGTGGATGA CAGTGCAGAA | 840 |
| TTTAAATGTG AGGCCCAGAG TGACCCTGTA CCTACAGTAC GATGGAGGAA AGATGATGGA | 900 |
| GAGCTGCCCA AATCCAGATA TGAAATCCGA GATGATCATA CCTTGAAAAT TAGGAAGGTG | 960 |
| ACAGCTGGTG ACATGGGTTC ATACACTTGT GTTGCAGAAA ATATGGTGGG CAAAGCTGAA | 1020 |
| GCATCTGCTA CTCTGACTGT TCAAGAACCT CCACATTTTG TTGTGAAACC CCGTGACCAG | 1080 |
| GTTGTTGCTT TGGGACGGAC TGTAACCTTT CAGTGTGAAG CAACCGGAAA TCCTCAACCA | 1140 |
| GCTATTTTCT GGAGGAGAGA AGGGAGTCAG AATCTACTTT TCTCATATCA ACCACCACAG | 1200 |
| TCATCCAGCC GATTTTCAGT CTCCCAGACT GGCGACCTCA CAATTACTAA TGTCCAGCGA | 1260 |
| TCTGATGTTG GTTATTACAT CTGCCAGACT TTAAATGTTG CTGGAAGCAT CATCACAAG | 1320 |
| GCATATTTGG AAGTTACAGA TGTGATTGCA GATCGGCCTC CCCCAGTTAT TCGACAAGGT | 1380 |

| | | | | | | |
|-------------|------------|-------------|------------|-------------|------------|------|
| CCTGTGAATC | AGACTGTAGC | CGTGGATGGC | ACTTTCGTCC | TCAGCTGTGT | GGCCACAGGC | 1440 |
| AGTCCAGTGC | CCACCATTCT | GTGGAGAAAG | GATGGAGTCC | TCGTTTCAAC | CCAAGACTCT | 1500 |
| CGAATCAAAC | AGTTGGAGAA | TGGAGTACTG | CAGATCCGAT | ATGCTAAGCT | GGGTGATACT | 1560 |
| GGTCGGTACA | CCTGCATTGC | ATCAACCCCC | AGTGGTGAAG | CAACATGGAG | TGCTTACATT | 1620 |
| GAAGTTCAAG | AATTTGGAGT | TCCAGTTCAG | CCTCCAAGAC | CTACTGACCC | AAATTTAATC | 1680 |
| CCTAGTGCCC | CATCAAAACC | TGAAGTGACA | GATGTCAGCA | GAAATACAGT | CACATTATCG | 1740 |
| TGGCAACCAA | ATTTGAATTC | AGGAGCAACT | CCAACATCTT | ATATTATAGA | AGCCTTCAGC | 1800 |
| CATGCATCTG | GTAGCAGCTG | GCAGACCGTA | GCAGAGAATG | TGAAAACAGA | AACATCTGCC | 1860 |
| ATTAAAGGAC | TCAAACCTAA | TGCAATTTAC | CTTTTCCTTG | TGAGGGCAGC | TAATGCATAT | 1920 |
| GGAATTAGTG | ATCCAAGCCA | AATATCAGAT | CCAGTGAAAA | CACAAGATGT | CCTACCAACA | 1980 |
| AGTCAGGGGG | TGGACCACAA | GCAGGTCCAG | AGAGAGCTGG | GAAATGCTGT | TCTGCACCTC | 2040 |
| CACAACCCCA | CCGTCTTTTC | TTCCTCTTCC | ATCGAAGTGC | ACTGGACAGT | AGATCAACAG | 2100 |
| TCTCAGTATA | TACAAGGATA | TAAAATTCTC | TATCGGCCAT | CTGGAGCCAA | CCACGGAGAA | 2160 |
| TCAGACTGGT | TAGTTTTTGA | AGTGAGGACG | CCAGCCAAAA | ACAGTGTTGGT | AATCCCTGAT | 2220 |
| CTCAGAAAGG | GAGTCAACTA | TGAAATTAAG | GCTCGCCCTT | TTTTTAATGA | ATTTCAAGGA | 2280 |
| GCAGATAGTG | AAATCAAGTT | TGCCAAAACC | CTGGAAGAAG | CACCCAGTGC | CCCACCCCAA | 2340 |
| GGTGTAAC TG | TATCCAAGAA | TGATGGAAAC | GGAAGTGCAG | TTCTAGTTAG | TTGGCAGCCA | 2400 |
| CCTCCAGAAG | ACACTCAAAA | TGGAATGGTC | CAAGAGTATA | AGGTTTGGTG | TCTGGGCAAT | 2460 |
| GAAACTCGAT | ACCACATCAA | CAAAACAGTG | GATGGTTCCA | CCTTTTCCGT | GGTCATTCCC | 2520 |
| TTTCTTGTTT | CTGGAATCCG | ATACAGTGTG | GAAGTGGCAG | CCAGCACTGG | GGCTGGGTCT | 2580 |
| GGGGTAAAGA | GTGAGCCTCA | GTTTCATCCAG | CTGGATGCCC | ATGGAAACCC | TGTGTCACCT | 2640 |
| GAGGACCAAG | TCAGCCTCGC | TCAGCAGATT | TCAGATGTGG | TGAAGCAGCC | GGCCTTCATA | 2700 |
| GCAGGTATTG | GAGCAGCCTG | TTGGATCATC | CTCATGGTCT | TCAGCATCTG | GCTTTATCGA | 2760 |
| CACCGCAAGA | AGAGAAACGG | ACTTACTAGT | ACCTACGCGG | GTATCAGAAA | AGTCCCGTCT | 2820 |
| TTTACCTTCA | CACCAACAGT | AACTTACCAG | AGAGGAGGCG | AAGCTGTCAG | CAGTGAGGGG | 2880 |
| AGGCCTGGAC | TTCTCAACAT | CAGTGAACCT | GCCGCGCAGC | CATGGCTGGC | AGACACGTGG | 2940 |
| CCTAATACTG | GCAACAACCA | CAATGACTGC | TCCATCAGCT | GCTGCACGGC | AGGCAATGGA | 3000 |
| AACAGCGACA | GCAACCTCAC | TACCTACAGT | CGCCCAGCTG | ATTGTATAGC | AAATTATAAC | 3060 |
| AACCAACTGG | ATAACAAACA | AACAAATCTG | ATGCTCCCTG | AGTCAACTGT | TTATGGTGAT | 3120 |
| GTGGACCTTA | GTAACAAAAT | CAATGAGATG | AAAACCTTCA | ATAGCCCAAA | TCTGAAGGAT | 3180 |
| GGGCGTTTTG | TCAATCCATC | AGGGCAGCCT | ACTCCTTACG | CCACCACTCA | GCTCATCCAG | 3240 |
| TCAAACCTCA | GCAACAACAT | GAACAATGGC | AGCGGGGACT | CTGGCGAGAA | GCACTGGAAA | 3300 |
| CCACTGGGAC | AGCAGAAACA | AGAAGTGGCA | CCAGTTCAGT | ACAACATCGT | GGAGCAAAAC | 3360 |
| AAGCTGAACA | AAGATTATCG | AGCAAATGAC | ACAGTTCCTC | CAACTATCCC | ATACAACCAA | 3420 |
| TCATACGACC | AGAACACAGG | AGGATCCTAC | AACAGCTCAG | ACCGGGGCAG | TAGTACATCT | 3480 |
| GGGAGTCAGG | GGCACAAGAA | AGGGGCAAGA | ACACCCAAGG | TACCAAAACA | GGGTGGCATG | 3540 |
| AACTGGGCAG | ACCTGCTTCC | TCCTCCCCCA | GCACATCCTC | CTCCACACAG | CAATAGCGAA | 3600 |
| GAGTACAACA | TTTCTGTAGA | TGAAAGCTAT | GACCAAGAAA | TGCCATGTCC | CGTGCCACCA | 3660 |

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|------------|------------|-------------|------------|------------|------------|------|
| GCAAGGATGT | ATTTGCAACA | AGATGAATTA | GAAGAGGAGG | AAGATGAACG | AGGCCCCACT | 3720 |
| CCCCCTGTTC | GGGGAGCAGC | TTCTTCTCCA | GCTGCCGTGT | CCTATAGCCA | TCAGTCCACT | 3780 |
| GCCACTCTGA | CTCCCTCCCC | ACAGGAAGAA | CTCCAGCCCA | TGTTACAGGA | TTGTCCAGAG | 3840 |
| GAGACTGGCC | ACATGCAGCA | CCAGCCCCGAC | AGGAGACGGC | AGCCTGTGAG | TCCTCCTCCA | 3900 |
| CCACCACGGC | CGATCTCCCC | TCCACATACC | TATGGCTACA | TTTCAGGACC | CCTGGTCTCA | 3960 |
| GATATGGATA | CGGATGCGCC | AGAAGAGGAA | GAAGACGAAG | CCGACATGGA | GGTAGCCAAG | 4020 |
| ATGCAAACCA | GAAGGCTTTT | GTTACGTGGG | CTTGAGCAGA | CACCTGCCTC | CAGTGTGGG | 4080 |
| GACCTGGAGA | GCTCTGTCAC | GGGGTCCATG | ATCAACGGCT | GGGGCTCAGC | CTCAGAGGAG | 4140 |
| GACAACATTT | CCAGCGGACG | CTCCAGTGTT | AGTTCTTCGG | ACGGCTCCTT | TTTCACTGAT | 4200 |
| GCTGACTTTG | CCCAGGCAGT | CGCAGCAGCG | GCAGAGTATG | CTGGTCTGAA | AGTAGCACGA | 4260 |
| CGGCAAATGC | AGGATGCTGC | TGGCCGTCGA | CATTTTCATG | CGTCTCAGTG | CCCTAGGCCC | 4320 |
| ACAAGTCCCG | TGTCTACAGA | CAGCAACATG | AGTGCCGCCG | TAATGCAGAA | AACCAGACCA | 4380 |
| GCCAAGAAAC | TGAAACACCA | GCCAGGACAT | CTGCGCAGAG | AAACCTACAC | AGATGATCTT | 4440 |
| CCACCACCTC | CTGTGCCGCC | ACCTGCTATA | AAGTCACCTA | CTGCCCAATC | CAAGACACAG | 4500 |
| CTGGAAGTAC | GACCTGTAGT | GGTGCCAAAA | CTCCCTTCTA | TGGATGCAAG | AACAGACAGA | 4560 |
| TCATCAGACA | GAAAAGGAAG | CAGTTACAAG | GGGAGAGAAG | TGTTGGATGG | AAGACAGGTT | 4620 |
| GTTGACATGC | GAACAAATCC | AGGTGATCCC | AGAGAAGCAC | AGGAACAGCA | AAATGACGGG | 4680 |
| AAAGGACGTG | GAAACAAGGC | AGCAAAACGA | GACCTTCCAC | CAGCAAAGAC | TCATCTCATC | 4740 |
| CAAGAGGATA | TTCTACCTTA | TTGTAGACCT | ACTTTTCCAA | CATCAAATAA | TCCCAGAGAT | 4800 |
| CCCAGTTCCT | CAAGCTCAAT | GTCATCAAGA | GGATCAGGAA | GCAGACAAAG | AGAACAAGCA | 4860 |
| AATGTAGGTC | GAAGAAATAT | TGCAGAAATG | CAGGTACTTG | GAGGATATGA | AAGAGGAGAA | 4920 |
| GATAATAATG | AAGAATTAGA | GGAAACTGAA | AGCTGA | | | 4956 |

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1651 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Trp | Lys | His | Val | Pro | Phe | Leu | Val | Met | Ile | Ser | Leu | Leu | Ser |
| 1 | | | | 5 | | | | | | 10 | | | | 15 | |
| Leu | Ser | Pro | Asn | His | Leu | Phe | Leu | Ala | Gln | Leu | Ile | Pro | Asp | Pro | Glu |
| | | | | 20 | | | | | | 25 | | | | 30 | |
| Asp | Val | Glu | Arg | Gly | Asn | Asp | His | Gly | Thr | Pro | Ile | Pro | Thr | Ser | Asp |
| | | | | 35 | | | | | | 40 | | | | 45 | |
| Asn | Asp | Asp | Asn | Ser | Leu | Gly | Tyr | Thr | Gly | Ser | Arg | Leu | Arg | Gln | Glu |

| | | | | |
|---|-----|-----|-----|-----|
| 50 | | 55 | | 60 |
| Asp Phe Pro Pro Arg Ile Val Glu His Pro Ser Asp Leu Ile Val Ser | | | | |
| 65 | | 70 | | 75 |
| Lys Gly Glu Pro Ala Thr Leu Asn Cys Lys Ala Glu Gly Arg Pro Thr | | | | |
| | 85 | | 90 | 95 |
| Pro Thr Ile Glu Trp Tyr Lys Gly Gly Glu Arg Val Glu Thr Asp Lys | | | | |
| | 100 | | 105 | 110 |
| Asp Asp Pro Arg Ser His Arg Met Leu Leu Pro Ser Gly Ser Leu Phe | | | | |
| | 115 | | 120 | 125 |
| Phe Leu Arg Ile Val His Gly Arg Lys Ser Arg Pro Asp Glu Gly Val | | | | |
| | 130 | | 135 | 140 |
| Tyr Val Cys Val Ala Arg Asn Tyr Leu Gly Glu Ala Val Ser His Asn | | | | |
| 145 | | 150 | | 155 |
| Ala Ser Leu Glu Val Ala Ile Leu Arg Asp Asp Phe Arg Gln Asn Pro | | | | |
| | 165 | | 170 | 175 |
| Ser Asp Val Met Val Ala Val Gly Glu Pro Ala Val Met Glu Cys Gln | | | | |
| | 180 | | 185 | 190 |
| Pro Pro Arg Gly His Pro Glu Pro Thr Ile Ser Trp Lys Lys Asp Gly | | | | |
| | 195 | | 200 | 205 |
| Ser Pro Leu Asp Asp Lys Asp Glu Arg Ile Thr Ile Arg Gly Gly Lys | | | | |
| | 210 | | 215 | 220 |
| Leu Met Ile Thr Tyr Thr Arg Lys Ser Asp Ala Gly Lys Tyr Val Cys | | | | |
| 225 | | 230 | | 235 |
| Val Gly Thr Asn Met Val Gly Glu Arg Glu Ser Glu Val Ala Glu Leu | | | | |
| | 245 | | 250 | 255 |
| Thr Val Leu Glu Arg Pro Ser Phe Val Lys Arg Pro Ser Asn Leu Ala | | | | |
| | 260 | | 265 | 270 |
| Val Thr Val Asp Asp Ser Ala Glu Phe Lys Cys Glu Ala Arg Gly Asp | | | | |
| | 275 | | 280 | 285 |
| Pro Val Pro Thr Val Arg Trp Arg Lys Asp Asp Gly Glu Leu Pro Lys | | | | |
| | 290 | | 295 | 300 |
| Ser Arg Tyr Glu Ile Arg Asp Asp His Thr Leu Lys Ile Arg Lys Val | | | | |
| 305 | | 310 | | 315 |
| Thr Ala Gly Asp Met Gly Ser Tyr Thr Cys Val Ala Glu Asn Met Val | | | | |
| | 325 | | 330 | 335 |
| Gly Lys Ala Glu Ala Ser Ala Thr Leu Thr Val Gln Glu Pro Pro His | | | | |
| | 340 | | 345 | 350 |
| Phe Val Val Lys Pro Arg Asp Gln Val Val Ala Leu Gly Arg Thr Val | | | | |

| | | |
|---|-----------------------------|-------------|
| 355 | 360 | 365 |
| Thr Phe Gln Cys Glu Ala | Thr Gly Asn Pro Gln Pro Ala | Ile Phe Trp |
| 370 | 375 | 380 |
| Arg Arg Glu Gly Ser Gln Asn Leu Leu Phe Ser Tyr Gln Pro Pro Gln | | |
| 385 | 390 | 395 |
| 400 | | |
| Ser Ser Ser Arg Phe Ser Val Ser Gln Thr Gly Asp Leu Thr Ile Thr | | |
| 405 | 410 | 415 |
| Asn Val Gln Arg Ser Asp Val Gly Tyr Tyr Ile Cys Gln Thr Leu Asn | | |
| 420 | 425 | 430 |
| Val Ala Gly Ser Ile Ile Thr Lys Ala Tyr Leu Glu Val Thr Asp Val | | |
| 435 | 440 | 445 |
| Ile Ala Asp Arg Pro Pro Pro Val Ile Arg Gln Gly Pro Val Asn Gln | | |
| 450 | 455 | 460 |
| Thr Val Ala Val Asp Gly Thr Phe Val Leu Ser Cys Val Ala Thr Gly | | |
| 465 | 470 | 475 |
| 480 | | |
| Ser Pro Val Pro Thr Ile Leu Trp Arg Lys Asp Gly Val Leu Val Ser | | |
| 485 | 490 | 495 |
| Thr Gln Asp Ser Arg Ile Lys Gln Leu Glu Asn Gly Val Leu Gln Ile | | |
| 500 | 505 | 510 |
| Arg Tyr Ala Lys Leu Gly Asp Thr Gly Arg Tyr Thr Cys Ile Ala Ser | | |
| 515 | 520 | 525 |
| Thr Pro Ser Gly Glu Ala Thr Trp Ser Ala Tyr Ile Glu Val Gln Glu | | |
| 530 | 535 | 540 |
| Phe Gly Val Pro Val Gln Pro Pro Arg Pro Thr Asp Pro Asn Leu Ile | | |
| 545 | 550 | 555 |
| 560 | | |
| Pro Ser Ala Pro Ser Lys Pro Glu Val Thr Asp Val Ser Arg Asn Thr | | |
| 565 | 570 | 575 |
| Val Thr Leu Ser Trp Gln Pro Asn Leu Asn Ser Gly Ala Thr Pro Thr | | |
| 580 | 585 | 590 |
| Ser Tyr Ile Ile Glu Ala Phe Ser His Ala Ser Gly Ser Ser Trp Gln | | |
| 595 | 600 | 605 |
| Thr Val Ala Glu Asn Val Lys Thr Glu Thr Ser Ala Ile Lys Gly Leu | | |
| 610 | 615 | 620 |
| Lys Pro Asn Ala Ile Tyr Leu Phe Leu Val Arg Ala Ala Asn Ala Tyr | | |
| 625 | 630 | 635 |
| 640 | | |
| Gly Ile Ser Asp Pro Ser Gln Ile Ser Asp Pro Val Lys Thr Gln Asp | | |
| 645 | 650 | 655 |
| Val Leu Pro Thr Ser Gln Gly Val Asp His Lys Gln Val Gln Arg Glu | | |

| | | |
|-------------------------|---|-------------|
| 660 | 665 | 670 |
| Leu Gly Asn Ala Val | Leu His Leu His Asn Pro Thr Val | Leu Ser Ser |
| 675 | 680 | 685 |
| Ser Ser Ile Glu Val | His Trp Thr Val Asp Gln Gln Ser | Gln Tyr Ile |
| 690 | 695 | 700 |
| Gln Gly Tyr Lys Ile | Leu Tyr Arg Pro Ser Gly Ala Asn His Gly Glu | |
| 705 | 710 | 715 |
| Ser Asp Trp Leu Val | Phe Glu Val Arg Thr Pro Ala Lys Asn Ser Val | |
| 725 | 730 | 735 |
| Val Ile Pro Asp Leu Arg | Lys Gly Val Asn Tyr Glu Ile Lys Ala Arg | |
| 740 | 745 | 750 |
| Pro Phe Phe Asn Glu Phe | Gln Gly Ala Asp Ser Glu Ile Lys Phe Ala | |
| 755 | 760 | 765 |
| Lys Thr Leu Glu Glu Ala | Pro Ser Ala Pro Pro Gln Gly Val Thr Val | |
| 770 | 775 | 780 |
| Ser Lys Asn Asp Gly Asn | Gly Thr Ala Ile Leu Val Ser Trp Gln Pro | |
| 785 | 790 | 795 |
| Pro Pro Glu Asp Thr Gln | Asn Gly Met Val Gln Glu Tyr Lys Val Trp | |
| 805 | 810 | 815 |
| Cys Leu Gly Asn Glu Thr | Arg Tyr His Ile Asn Lys Thr Val Asp Gly | |
| 820 | 825 | 830 |
| Ser Thr Phe Ser Val Val | Ile Pro Phe Leu Val Pro Gly Ile Arg Tyr | |
| 835 | 840 | 845 |
| Ser Val Glu Val Ala Ala | Ser Thr Gly Ala Gly Ser Gly Val Lys Ser | |
| 850 | 855 | 860 |
| Glu Pro Gln Phe Ile Gln | Leu Asp Ala His Gly Asn Pro Val Ser Pro | |
| 865 | 870 | 875 |
| Glu Asp Gln Val Ser Leu | Ala Gln Gln Ile Ser Asp Val Val Lys Gln | |
| 885 | 890 | 895 |
| Pro Ala Phe Ile Ala Gly | Ile Gly Ala Ala Cys Trp Ile Ile Leu Met | |
| 900 | 905 | 910 |
| Val Phe Ser Ile Trp Leu | Tyr Arg His Arg Lys Lys Arg Asn Gly Leu | |
| 915 | 920 | 925 |
| Thr Ser Thr Tyr Ala Gly | Ile Arg Lys Val Pro Ser Phe Thr Phe Thr | |
| 930 | 935 | 940 |
| Pro Thr Val Thr Tyr Gln | Arg Gly Gly Glu Ala Val Ser Ser Gly Gly | |
| 945 | 950 | 955 |
| Arg Pro Gly Leu Leu Asn | Ile Ser Glu Pro Ala Ala Gln Pro Trp Leu | |

| | | |
|---|------|------|
| 965 | 970 | 975 |
| Ala Asp Thr Trp Pro Asn Thr Gly Asn Asn His Asn Asp Cys Ser Ile | | |
| 980 | 985 | 990 |
| Ser Cys Cys Thr Ala Gly Asn Gly Asn Ser Asp Ser Asn Leu Thr Thr | | |
| 995 | 1000 | 1005 |
| Tyr Ser Arg Pro Ala Asp Cys Ile Ala Asn Tyr Asn Asn Gln Leu Asp | | |
| 1010 | 1015 | 1020 |
| Asn Lys Gln Thr Asn Leu Met Leu Pro Glu Ser Thr Val Tyr Gly Asp | | |
| 1025 | 1030 | 1035 |
| Val Asp Leu Ser Asn Lys Ile Asn Glu Met Lys Thr Phe Asn Ser Pro | | 1040 |
| 1045 | 1050 | 1055 |
| Asn Leu Lys Asp Gly Arg Phe Val Asn Pro Ser Gly Gln Pro Thr Pro | | |
| 1060 | 1065 | 1070 |
| Tyr Ala Thr Thr Gln Leu Ile Gln Ser Asn Leu Ser Asn Asn Met Asn | | |
| 1075 | 1080 | 1085 |
| Asn Gly Ser Gly Asp Ser Gly Glu Lys His Trp Lys Pro Leu Gly Gln | | |
| 1090 | 1095 | 1100 |
| Gln Lys Gln Glu Val Ala Pro Val Gln Tyr Asn Ile Val Glu Gln Asn | | |
| 1105 | 1110 | 1115 |
| Lys Leu Asn Lys Asp Tyr Arg Ala Asn Asp Thr Val Pro Pro Thr Ile | | 1120 |
| 1125 | 1130 | 1135 |
| Pro Tyr Asn Gln Ser Tyr Asp Gln Asn Thr Gly Gly Ser Tyr Asn Ser | | |
| 1140 | 1145 | 1150 |
| Ser Asp Arg Gly Ser Ser Thr Ser Gly Ser Gln Gly His Lys Lys Gly | | |
| 1155 | 1160 | 1165 |
| Ala Arg Thr Pro Lys Val Pro Lys Gln Gly Gly Met Asn Trp Ala Asp | | |
| 1170 | 1175 | 1180 |
| Leu Leu Pro Pro Pro Pro Ala His Pro Pro Pro His Ser Asn Ser Glu | | |
| 1185 | 1190 | 1195 |
| Glu Tyr Asn Ile Ser Val Asp Glu Ser Tyr Asp Gln Glu Met Pro Cys | | 1200 |
| 1205 | 1210 | 1215 |
| Pro Val Pro Pro Ala Arg Met Tyr Leu Gln Gln Asp Glu Leu Glu Glu | | |
| 1220 | 1225 | 1230 |
| Glu Glu Asp Glu Arg Gly Pro Thr Pro Pro Val Arg Gly Ala Ala Ser | | |
| 1235 | 1240 | 1245 |
| Ser Pro Ala Ala Val Ser Tyr Ser His Gln Ser Thr Ala Thr Leu Thr | | |
| 1250 | 1255 | 1260 |
| Pro Ser Pro Gln Glu Glu Leu Gln Pro Met Leu Gln Asp Cys Pro Glu | | |

| | | | |
|---|------|------|------|
| 1265 | 1270 | 1275 | 1280 |
| Glu Thr Gly His Met Gln His Gln Pro Asp Arg Arg Arg Gln Pro Val | | | |
| | 1285 | 1290 | 1295 |
| Ser Pro Pro Pro Pro Pro Arg Pro Ile Ser Pro Pro His Thr Tyr Gly | | | |
| | 1300 | 1305 | 1310 |
| Tyr Ile Ser Gly Pro Leu Val Ser Asp Met Asp Thr Asp Ala Pro Glu | | | |
| | 1315 | 1320 | 1325 |
| Glu Glu Glu Asp Glu Ala Asp Met Glu Val Ala Lys Met Gln Thr Arg | | | |
| | 1330 | 1335 | 1340 |
| Arg Leu Leu Leu Arg Gly Leu Glu Gln Thr Pro Ala Ser Ser Val Gly | | | |
| 1345 | 1350 | 1355 | 1360 |
| Asp Leu Glu Ser Ser Val Thr Gly Ser Met Ile Asn Gly Trp Gly Ser | | | |
| | 1365 | 1370 | 1375 |
| Ala Ser Glu Glu Asp Asn Ile Ser Ser Gly Arg Ser Ser Val Ser Ser | | | |
| | 1380 | 1385 | 1390 |
| Ser Asp Gly Ser Phe Phe Thr Asp Ala Asp Phe Ala Gln Ala Val Ala | | | |
| | 1395 | 1400 | 1405 |
| Ala Ala Ala Glu Tyr Ala Gly Leu Lys Val Ala Arg Arg Gln Met Gln | | | |
| | 1410 | 1415 | 1420 |
| Asp Ala Ala Gly Arg Arg His Phe His Ala Ser Gln Cys Pro Arg Pro | | | |
| 1425 | 1430 | 1435 | 1440 |
| Thr Ser Pro Val Ser Thr Asp Ser Asn Met Ser Ala Ala Val Met Gln | | | |
| | 1445 | 1450 | 1455 |
| Lys Thr Arg Pro Ala Lys Lys Leu Lys His Gln Pro Gly His Leu Arg | | | |
| | 1460 | 1465 | 1470 |
| Arg Glu Thr Tyr Thr Asp Asp Leu Pro Pro Pro Pro Val Pro Pro Pro | | | |
| | 1475 | 1480 | 1485 |
| Ala Ile Lys Ser Pro Thr Ala Gln Ser Lys Thr Gln Leu Glu Val Arg | | | |
| | 1490 | 1495 | 1500 |
| Pro Val Val Val Pro Lys Leu Pro Ser Met Asp Ala Arg Thr Asp Arg | | | |
| 1505 | 1510 | 1515 | 1520 |
| Ser Ser Asp Arg Lys Gly Ser Ser Tyr Lys Gly Arg Glu Val Leu Asp | | | |
| | 1525 | 1530 | 1535 |
| Gly Arg Gln Val Val Asp Met Arg Thr Asn Pro Gly Asp Pro Arg Glu | | | |
| | 1540 | 1545 | 1550 |
| Ala Gln Glu Gln Gln Asn Asp Gly Lys Gly Arg Gly Asn Lys Ala Ala | | | |
| | 1555 | 1560 | 1565 |
| Lys Arg Asp Leu Pro Pro Ala Lys Thr His Leu Ile Gln Glu Asp Ile | | | |

| | | | |
|---|------|------|------|
| 1570 | 1575 | 1580 | |
| Leu Pro Tyr Cys Arg Pro Thr Phe Pro Thr Ser Asn Asn Pro Arg Asp | | | |
| 1585 | 1590 | 1595 | 1600 |
| Pro Ser Ser Ser Ser Ser Met Ser Ser Arg Gly Ser Gly Ser Arg Gln | | | |
| | 1605 | 1610 | 1615 |
| Arg Glu Gln Ala Asn Val Gly Arg Arg Asn Ile Ala Glu Met Gln Val | | | |
| | 1620 | 1625 | 1630 |
| Leu Gly Gly Tyr Glu Arg Gly Glu Asp Asn Asn Glu Glu Leu Glu Glu | | | |
| | 1635 | 1640 | 1645 |
| Thr Glu Ser | | | |
| 1650 | | | |

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 855..1187
- (D) OTHER INFORMATION: /note= "N signifies gap in sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

| | |
|---|-----|
| CAGATTGTTG CTCAAGGTCG AACAGTGACA TTTCCCTGTG AAAGTAAAGG AAACCCACAG | 60 |
| CCAGCTGTTT TTTGGCAGAA AGAAGGCAGC CAGAACCTAC TTTTCCCAA CCAACCCAG | 120 |
| CAGCCCAACA GTAGATGCTC AGTGTCACCA ACTGGAGACC TCACAATCAC CAACATTCAA | 180 |
| CGTTCCGACG CGGGTTACTA CATCTGCCAG GCTTTAACTG TGGCAGGAAG CATTTTAGCA | 240 |
| AAAGCTCAAC TGGAGGTTAC TGATGTTTTG ACAGATAGAC CTCCACCTAT AATTCTACAA | 300 |
| GGCCCAGCCA ACCAAACGCT GGCAGTGGAT GGTACAGCGT TACTGAAATG TAAAGCCACT | 360 |
| GGTGATCCTC TTCCTGTAAT TAGCTGGTTA AAGGAGGGAT TTACTTTTCC GGGTAGAGAT | 420 |
| CCAAGAGCAA CAATTCAAGA GCAAGGCACA CTGCAGATTA AGAATTTACG GATTTCTGAT | 480 |
| ACTGGCACTT ATACTTGTGT GGCTACAAGT TCAAGTGGAG AGGCTTCCTG GAGTGCAGTG | 540 |
| CTGGATGTGA CAGAGTCTGG AGCAACAATC AGTAAAACT ATGATTTAAG TGACCTGCCA | 600 |
| GGGCCACCAT CCAAACGCA AGTCACTGAT GTTACTAAGA ACAGTGTAC CTTGTCCTGG | 660 |
| CAGCCAGGTA CCCCTGGAAC CCTTCCAGCA AGTGCATATA TCATTGAGGC TTTCAGCCAA | 720 |
| TCAGTGAGCA ACAGCTGGCA GACCGTGGCA AACCATGTAA AGACCACCCT CTATACTGTA | 780 |
| AGAGGACTGC GGCCCAATAC AATCTACTTA TTCATGGTCA GAGCGATCAA CCCCAAGGTY | 840 |

| | |
|---|------|
| TCAGTGACCC AAGTNAACC ACAGAAAAAC AATGGATCCA CTTGGGCCAA TGTCCCTCTA | 900 |
| CCTCCCCCCC CAGTCCAGCC CCTTCCTGGC ACGGAGCTGG AACACTATGC AGTGGAACAA | 960 |
| CAAGAAAATG GCTATGACAG TGATAGCTGG TGCCCACCAT TGCCAGTACA AACTTACTTA | 1020 |
| CACCAAGGTC TGGAAGATGA ACTGGAAGAA GATGATGATA GGGTCCCAAC ACCTCCTGTT | 1080 |
| CGAGGCGTGG CTTCTTCTCC TGCTATCTCC TTTGGACAGC AGTCCACTGC AACTCTTACT | 1140 |
| CCATCCCCAC GGGAAGAGAT GCAACCCATG CTGCAGGCTT CACCTNNTTA CCTCCTCTCA | 1200 |
| AAGACCTCGA CCTACCAGCC CATTTTCTAC TGACAGTAAC ACCAGTGCAG CCCTGAGTCA | 1260 |
| AAGTCAGAGG CCTCGGCCCA CTAAAAAACA CAAGGGAGGG | 1300 |

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 285..396
- (D) OTHER INFORMATION: /note= "Xaa signifies gap in sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Ile | Val | Ala | Gln | Gly | Arg | Thr | Val | Thr | Phe | Pro | Cys | Glu | Thr | Lys |
| 1 | | | | 5 | | | | | | 10 | | | | | 15 |
| Gly | Asn | Pro | Gln | Pro | Ala | Val | Phe | Trp | Gln | Lys | Glu | Gly | Ser | Gln | Asn |
| | | | | 20 | | | | | | 25 | | | | | 30 |
| Leu | Leu | Phe | Pro | Asn | Gln | Pro | Gln | Gln | Pro | Asn | Ser | Arg | Cys | Ser | Val |
| | | | | 35 | | | | | | 40 | | | | | 45 |
| Ser | Pro | Thr | Gly | Asp | Leu | Thr | Ile | Thr | Asn | Ile | Gln | Arg | Ser | Asp | Ala |
| | | | | 50 | | | | | | 55 | | | | | 60 |
| Gly | Tyr | Tyr | Ile | Cys | Gln | Ala | Leu | Thr | Val | Ala | Gly | Ser | Ile | Leu | Ala |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Lys | Ala | Gln | Leu | Glu | Val | Thr | Asp | Val | Leu | Thr | Asp | Arg | Pro | Pro | Pro |
| | | | | 85 | | | | | | 90 | | | | | 95 |
| Ile | Ile | Leu | Gln | Gly | Pro | Ala | Asn | Gln | Thr | Leu | Ala | Val | Asp | Gly | Thr |
| | | | | 100 | | | | | | 105 | | | | | 110 |
| Ala | Leu | Leu | Lys | Cys | Lys | Ala | Thr | Gly | Asp | Pro | Leu | Pro | Val | Ile | Ser |
| | | | | 115 | | | | | | 120 | | | | | 125 |
| Trp | Leu | Lys | Glu | Gly | Phe | Thr | Phe | Pro | Gly | Arg | Asp | Pro | Arg | Ala | Thr |

| | | | |
|---|-----|-----|-----|
| 130 | 135 | 140 | |
| Ile Gln Glu Gln Gly Thr Leu Gln Ile Lys Asn Leu Arg Ile Ser Asp | | | |
| 145 | 150 | 155 | 160 |
| Thr Gly Thr Tyr Thr Cys Val Ala Thr Ser Ser Ser Gly Glu Ala Ser | | | |
| | 165 | 170 | 175 |
| Trp Ser Ala Val Leu Asp Val Thr Glu Ser Gly Ala Thr Ile Ser Lys | | | |
| | 180 | 185 | 190 |
| Asn Tyr Asp Leu Ser Asp Leu Pro Gly Pro Pro Ser Lys Pro Gln Val | | | |
| | 195 | 200 | 205 |
| Thr Asp Val Thr Lys Asn Ser Val Thr Leu Ser Trp Gln Pro Gly Thr | | | |
| | 210 | 215 | 220 |
| Pro Gly Thr Leu Pro Ala Ser Ala Tyr Ile Ile Glu Ala Phe Ser Gln | | | |
| 225 | 230 | 235 | 240 |
| Ser Val Ser Asn Ser Trp Gln Thr Val Ala Asn His Val Lys Thr Thr | | | |
| | 245 | 250 | 255 |
| Leu Tyr Thr Val Arg Gly Leu Arg Pro Asn Thr Ile Tyr Leu Phe Met | | | |
| | 260 | 265 | 270 |
| Val Arg Ala Ile Asn Pro Lys Val Ser Val Thr Gln Xaa Lys Pro Gln | | | |
| | 275 | 280 | 285 |
| Lys Asn Asn Gly Ser Thr Trp Ala Asn Val Pro Leu Pro Pro Pro Pro | | | |
| | 290 | 295 | 300 |
| Val Gln Pro Leu Pro Gly Thr Glu Leu Glu His Tyr Ala Val Glu Gln | | | |
| 305 | 310 | 315 | 320 |
| Gln Glu Asn Gly Tyr Asp Ser Asp Ser Trp Cys Pro Pro Leu Pro Val | | | |
| | 325 | 330 | 335 |
| Gln Thr Tyr Leu His Gln Gly Leu Glu Asp Glu Leu Glu Glu Asp Asp | | | |
| | 340 | 345 | 350 |
| Asp Arg Val Pro Thr Pro Pro Val Arg Gly Val Ala Ser Ser Pro Ala | | | |
| | 355 | 360 | 365 |
| Ile Ser Phe Gly Gln Gln Ser Thr Ala Thr Leu Thr Pro Ser Pro Arg | | | |
| | 370 | 375 | 380 |
| Glu Glu Met Gln Pro Met Leu Gln Ala Ser Pro Xaa Phe Thr Ser Ser | | | |
| 385 | 390 | 395 | 400 |
| Gln Arg Pro Arg Pro Thr Ser Pro Phe Ser Thr Asp Ser Asn Thr Ser | | | |
| | 405 | 410 | 415 |
| Ala Ala Leu Ser Gln Ser Gln Arg Pro Arg Pro Thr Lys Lys His Lys | | | |
| | 420 | 425 | 430 |
| Gly Gly | | | |

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

| | |
|---|-----|
| GCCCAGGCAG TTGCTGCAGC TCGGAGTAT GCGGGCCTGA AAGTGGCTCG CCGCCAAATG | 60 |
| CAAGATGCTG CTGGCCGCCG CCACTTCCAT GCCTCTCAGT GCCCAAGGCC CACGAGTCCT | 120 |
| GTGTCCACAG ACAGCAACAT GAGTGCTGTT GTGATCCAGA AAGCCAGACC CGCCAAGAAG | 180 |
| CAGAAACACC AGCCAGGACA TCTGCGCAGG GAAGCCTACG CAGATGATCT TCCACCCCCT | 240 |
| CCAGTGCCAC CACCTGCTAT AAAATCGCCC ACTGTCCAGT CCAAGGCACA GCTGGAGGTA | 300 |
| CGGCCTGTCA TGGTGCCAAA ACTCGCGTCT ATAGAAGCAA GGACAGATAG ATCGTCAGAC | 360 |
| AGAAAAGGAG GCAGTTACAA GGGGAGAGAA GCTCTGGATG GAAGACAAGT CACTGACCTG | 420 |
| CGAACAAATC CAAGTGACCC CAGA | 444 |

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

| | |
|---|----------|
| Ala Gln Ala Val Ala Ala Ala Ala Glu Tyr Ala Gly Leu Lys Val Ala | |
| 1 | 5 10 15 |
| Arg Arg Gln Met Gln Asp Ala Ala Gly Arg Arg His Phe His Ala Ser | |
| 20 | 25 30 |
| Gln Cys Pro Arg Pro Thr Ser Pro Val Ser Thr Asp Ser Asn Met Ser | |
| 35 | 40 45 |
| Ala Val Val Ile Gln Lys Ala Arg Pro Ala Lys Lys Gln Lys His Gln | |
| 50 | 55 60 |
| Pro Gly His Leu Arg Arg Glu Ala Tyr Ala Asp Asp Leu Pro Pro Pro | |
| 65 | 70 75 80 |
| Pro Val Pro Pro Pro Ala Ile Lys Ser Pro Thr Val Gln Ser Lys Ala | |
| 85 | 90 95 |

Gln Leu Glu Val Arg Pro Val Met Val Pro Lys Leu Ala Ser Ile Glu
 100 105 110
 Ala Arg Thr Asp Arg Ser Ser Asp Arg Lys Gly Gly Ser Tyr Lys Gly
 115 120 125
 Arg Glu Ala Leu Asp Gly Arg Gln Val Thr Asp Leu Arg Thr Asn Pro
 130 135 140
 Ser Asp Pro Arg
 145